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(54) Title: LACCASE MUTANTS (57) Abstract The present invention relates to a method of designing laccase mutants with improved stability properties, which method is based on the hitherto unknown three-dimensional structure of <i>Coprinus cinereus</i> laccase.		

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LACCASE MUTANTS

FIELD OF THE INVENTION

5 The present invention relates to a method of designing laccase mutants with improved stability properties, which method is based on the hitherto unknown three-dimensional structure of laccases.

10 BACKGROUND OF THE INVENTION

Laccase is a polyphenol oxidase (EC 1.10.3.2) which catalyses the oxidation of a variety of inorganic and aromatic compounds, particularly phenols, with the concomitant reduction of molecular
15 oxygen to water.

Laccase belongs to a family of blue copper-containing oxidases which includes ascorbate oxidase and the mammalian plasma protein ceruloplasmin. All these enzymes are multi-copper-containing proteins.

20 Because laccases are able to catalyze the oxidation of a variety of inorganic and aromatic compounds, laccases have been suggested in many potential industrial applications such as lignin modification, paper strengthening, dye transfer inhibition in detergents, phenol polymerization, hair colouring, and waste
25 water treatment. A major problem with the use of laccases are their poor storage stability at temperatures above room temperature, especially at 40°C.

In Example 1 of the present application we have tested the stability of various laccases at 40°C, and it can be seen that
30 after 2 weeks of storage the laccase activity is down to less than 50% of the initial value, and at low pH the laccase activity after 2 weeks is zero. For many purposes such a decrease is unacceptable, so it is the purpose of the present invention to create laccase variants with improved stability by using the
35 information of a three-dimensional structure of a *Coprinus cinereus* laccase. No three-dimensional structural information has been available for a laccase before.

BRIEF DISCLOSURE OF THE INVENTION

The three-dimensional structure of a laccase has now been elucidated. On the basis of an analysis of said structure it is possible to identify structural parts or specific amino acid residues which from structural or functional considerations appear to be important for the stability of a laccase.

Furthermore, when comparing the three-dimensional structure of the *Coprinus* laccase structure with known amino acid sequences of various laccases, it has been found that some similarities exist between the sequences. The present invention is based on these findings.

Accordingly, in a first aspect the invention relates to a method of constructing a variant of a parent *Coprinus* laccase, which variant has laccase activity and improved stability as compared to said parent laccase, which method comprises

i) analysing the three-dimensional structure of the parent *Coprinus* laccase to identify at least one amino acid residue or at least one structural part of the *Coprinus* laccase structure, which amino acid residue or structural part is believed to be of relevance for altering the stability of the parent *Coprinus* laccase (as evaluated on the basis of structural or functional considerations),

25

ii) constructing a *Coprinus* laccase variant, which as compared to the parent *Coprinus* laccase, has been modified in the amino acid residue or structural part identified in i) so as to alter the stability, and, optionally,

30

iii) testing the resulting *Coprinus* laccase variant with respect to stability.

In a second aspect the present invention relates to a method of constructing a variant of a parent *Coprinus*-like laccase, which variant has laccase activity and improved stability as compared to said parent laccase, which method comprises

i) comparing the three-dimensional amino acid structure of the

Coprinus laccase with an amino acid sequence of a *Coprinus*-like laccase,

- ii) identifying a part of the *Coprinus*-like laccase amino acid sequence which is different from the *Coprinus* laccase amino acid sequence and which from structural or functional considerations is contemplated to be responsible for differences in the stability of the *Coprinus* and *Coprinus*-like laccase,
- 10 iii) modifying the part of the *Coprinus*-like laccase identified in ii) whereby a *Coprinus*-like laccase variant is obtained, which has an improved stability as compared to the parent *Coprinus*-like laccase, and optionally,
- 15 iv) testing the resulting *Coprinus*-like laccase variant with respect to stability.

In still further aspects the invention relates to variants of a *Coprinus* laccase and of *Coprinus*-like laccases, DNA encoding
20 such variants and methods of preparing the variants. Finally, the invention relates to the use of the variants for various industrial purposes.

DETAILED DISCLOSURE OF THE INVENTION

25

The *Coprinus*-like laccases

A number of laccases produced by different fungi are homologous on the amino acid level. For instance, when using the homology percent obtained from UWGCG program using the GAP
30 program with the default parameters (penalties: gap weight=3.0, length weight=0.1; WISCONSIN PACKAGE Version 8.1-UNIX, August 1995, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711) the following homology was found:

Coprinus cinereus laccase comprising the amino acid sequence
35 shown in SEQ ID No. 1: 100%;

Polyporus pinsitus (I) laccase comprising the amino acid sequence

shown in SEQ ID No. 2: 74.4%;

Polyporus pinsitus (II) laccase comprising the amino acid sequence shown in SEQ ID No. 3: 73.8%;

Phlebia radiata laccase comprising the amino acid sequence shown
5 in SEQ ID No. 4: 69.9% ;

Rhizoctonia solani (I) laccase comprising the amino acid sequence shown in SEQ ID No. 5: 64.8%;

Rhizoctonia solani (II) laccase comprising the amino acid sequence shown in SEQ ID No. 6: 63.0%;

10 *Rhizoctonia solani* (III) laccase comprising the amino acid sequence shown in SEQ ID No. 7: 61.0%;

Rhizoctonia solani (IV) laccase comprising the amino acid sequence shown in SEQ ID No. 8: 59.7%;

Scytalidium thermophilum laccase comprising the amino acid
15 sequence shown in SEQ ID No. 9: 57.4%;

Myceliophthora thermophila laccase comprising the amino acid sequence shown in SEQ ID No. 10: 56.5%.

Because of the homology found between the above mentioned
20 laccases, they are considered to belong to the same class of laccases, namely the class of "Coprinus-like laccases".

Accordingly, in the present context, the term "Coprinus-like laccase" is intended to indicate a laccase which, on the amino acid level, displays a homology of at least 50% and less than
25 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or at least 55% and less than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or at least 60% and less than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or at least 65% and less than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or at least 70% and less
30 than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or at least 75% and less than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or at least 80% and less than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or at least 85% and less than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or at least 90% and
35 less than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1, or

at least 95% and less than 100% to the *Coprinus cinereus* laccase SEQ ID NO 1.

In the present context, "derived from" is intended not only to indicate a laccase produced or producible by a strain of the organism in question, but also a laccase encoded by a DNA sequence isolated from such strain and produced in a host organism containing said DNA sequence. Finally, the term is intended to indicate a laccase which is encoded by a DNA sequence of synthetic and/or cDNA origin and which has the identifying characteristics of the laccase in question.

The three-dimensional *Coprinus* laccase structure

The *Coprinus* laccase which was used to elucidate the three-dimensional structure forming the basis for the present invention consists of the 539 amino acids derived from *Coprinus cinereus* laccase IFO 8371 as disclosed in sequence ID No. 1.

The obtained three-dimensional structure is believed to be representative for the structure of any *Coprinus*-like laccase.

The structure of the laccase was solved in accordance with the principle for X-ray crystallographic methods given in "X-Ray Structure Determination", Stout, G.K. and Jensen, L.H., John Wiley & Sons, inc. NY, 1989. The structural coordinates for the solved crystal structure of the laccase at 2.2 Å resolution using the isomorphous replacement method are given in a standard PDB format (Brookhaven Protein Data Base) in Appendix 1. It is to be understood that Appendix 1 forms part of the present application.

In Appendix 1 the amino acid residues of the enzyme are identified by three-letter amino acid code (capitalized letters).

The laccase structure is made up of three plastocyanin-like domains. These three domains all have a similar beta-barrel fold.

3 copper atoms were observed in the three-dimensional structure:

The so-called type 1 copper ion is coordinated by two histidines and one cysteine.

The so-called type 2 copper of the trinuclear centre is missing in the structure disclosed in the present application.

The so-called type 3 copper consists of two type 3 copper

atoms (pair of copper atoms) bound to a total of 6 histidine ligands.

When comparing the amino acid sequence of the crystallized three-dimensional structure with *Coprinus cinereus* amino acid sequence ID No. 1 the following four differences are observed:

- 18 amino acids are missing from the N-terminal of the crystallized protein;
- 17 amino acids are missing from the C-terminal of the crystallized protein;
- Q19 in sequence ID No. 1 is an A1 in the crystallized protein; and
- Q243 in sequence ID No. 1 is an E225 in the crystallized protein.

Generality of structure

Because of the homology between the *Coprinus* laccase and the various *Coprinus*-like laccases, the solved structure defined by the coordinates of Appendix 1 is believed to be representative for the structure of all *Coprinus*-like laccases. A model structure of *Coprinus*-like laccases may be built on the basis of the coordinates given in Appendix 1 adapted to the laccase in question by use of an alignment between the respective amino acid sequences.

The above identified structurally characteristic parts of the *Coprinus* laccase structure may be identified in other *Coprinus*-like laccases on the basis of a model (or solved) structure of the relevant *Coprinus*-like laccase or simply on the basis of an alignment between the amino acid sequence of the *Coprinus*-like laccase in question with that of the *Coprinus* laccase used herein for identifying the amino acid residues of the respective structural elements.

Furthermore, in connection with *Coprinus* laccase variants of the invention, which are defined by modification of specific amino acid residues of the parent *Coprinus* laccase, it will be understood that variants of *Coprinus*-like laccases modified in an equivalent position (as determined from the best possible amino acid sequence alignment between the respective sequences) are

intended to be covered as well.

Methods of the invention for design of novel laccase variants

The analysis or comparison performed in step i) of the methods of the invention may be performed by use of any suitable computer programme capable of analysing and/or comparing amino acid sequences.

The structural part which is identified in step i) of the methods of the invention may be composed of one amino acid residue. However, normally the structural part comprises more than one amino acid residue, typically constituting one of the above mentioned parts of the *Coprinus* structure such as one of the copper centres.

According to the invention useful laccase variants may be modified in one or more amino acid residues present within 15 Å from any copper ion, preferably variants which are modified within 10 Å from any copper ion, in particular variants which are modified within 5 Å from any copper ion.

Determination of residues within 5Å, 10Å and 15Å from the copper ions in the three-dimensional structure: The coordinates from the appendix are read into INSIGHT program provided by BIOSYM technologies. The spatial coordinates are presented showing the bonds between the atoms. The copper atoms are presented as well as the water atoms. The program package contains a part which can be used for creating subsets. This part is used for creating a 5Å, 10Å and 15Å subset around all Cu-ions present in the structure (the command ZONE is used). The found subsets contain all residues having an atom within 5, 10 and 15Å from any of the Cu-ions present in the structure. All residues having an atom within this subset are compiled and written out by the LIST MOLECULE command.

The amino acid residues found in this way within a distance of 15 Å from a copper ion in the *Coprinus cinereus* laccase are the following (SEQ ID No 1 numbering):

M27, V46, G51, P52, I54, L64, L76, T79, S80, I81, H82, W83, H84, G85, L86, F87, Q88, R89, T91, N92, W93, A94, D95, G96, A97, D98, G99, V100, N101, Q102, C103, P104, Y113, F115, H120, G122, T123, F124, W125, Y126, H127, S128, H129, F130, G131, T132, Q133, Y134,

C135, D136, G137, L138, R139, G140, P141, M142, V143, I144, I164, T165, L166, A167, D168, H170, G179, A180, A181, Q182, P183, L217, I218, S219, L220, S221, C222, D223, P224, N225, W226, E239, V240, D241, G242, Q243, Q254, I255, F256, T257, G258, Q259, R260, Y261, 5 N281, K282, F349, Q350, L351, G352, F353, S354, G356, R357, F358, T359, I360, N361, T363, A364, Y365, E366, S367, P368, P371, T372, L373, P388, S391, V392, L403, V404, V405, P406, A407, G408, V409, L410, G411, G412, P413, H414, P415, F416, H417, L418, H419, G420, H421, A422, F423, A429, K441, R442, D443, V444, V445, S446, L447, 10 G448, V449, T450, D452, V454, I456, F458, N462, G464, P465, W466, F467, F468, H469, C470, H471, I472, E473, F474, H475, L476, M477, N478, G479, L480, A481, I482, V483, F484, A485, E486.

The amino acid residues found within a distance of 10 Å from a copper ion in the *Coprinus cinereus* laccase (SEQ ID No 1) are 15 the following:

S80, I81, H82, W83, H84, G85, L86, D95, G96, A97, D98, V100, N101, F124, W125, Y126, H127, S128, H129, F130, G131, Y134, L138, R139, G140,, I218, S219, L220, S221, C222, D223, P224, D241, F256, T257, G258, Q259, R260, K282, L351, G352, F353, F358, T359, 20 V405, V409, L410, G411, G412, P413, H414, P415, F416, H417, L418, H419, G420, D443, V444, V445, S446, L447, G448, V454, I456, F458, W466, F467, F468, H469, C470, H471, I472, E473, F474, H475, L476, M477, N478, G479, L480, A481, I482.

The amino acid residues found within a distance of 5 Å from a 25 copper ion in the *Coprinus cinereus* laccase (SEQ ID No 1) are the following:

H82, H84, W125, H127, H129, G411, H414, P415, H417, H419, F467, H469, C470, H471, I472, H475, L480.

The 15Å/10Å/5Å regions can be found in other laccases by 30 comparison of the modelled structures or by taking the sequence homology numbers.

Modifications

The modification of an amino acid residue or structural part 35 is typically accomplished by suitable modifications of a DNA sequence encoding the parent enzyme in question. The term "modified" as used in the methods according to the invention is intended to have the following meaning: When used in relation to

an amino acid residue the term is intended to mean replacement of the amino acid residue in question with another amino acid residue. When used in relation to a structural part, the term is intended to mean: replacement of one or more amino acid residues of said structural part with other amino acid residues, or addition of one or more amino acid residues to said part, or deletion of one or more amino acid residues of said structural part.

The construction of the variant of interest is accomplished by cultivating a microorganism comprising a DNA sequence encoding the variant under conditions which are conducive for producing the variant, and optionally subsequently recovering the variant from the resulting culture broth. This is described in detail further below.

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Variants with altered stability

It is contemplated that it is possible to improve the stability of a parent *Coprinus* laccase or a parent *Coprinus*-like laccase, wherein said variant is the result of a mutation, i.e. one or more amino acid residues having been deleted from, replaced or added to the parent laccase, the stability test performed as described below.

Preferred positions for mutations are the following:

25	MtL:	StL:	CcL:	PpL1:	PpL2:	PrL:	RsL4:	RsL1:	RsL2:	RsL3:
	M433	M483	-	-	-	-	-	-	-	-
	W373	W422	-	-	-	-	W411	W411	W439	-
	W136	W181	W125	W107	W107	W128	W125	W125	W125	W126
	Y145	Y190	Y134	Y116	Y116	Y137	Y134	Y134	Y134	Y135
30	M480	M530	-	-	-	-	-	-	-	-
	Y137	Y182	Y126	Y108	Y108	Y129	Y126	Y126	Y126	Y127
	Y176	Y221	Y170	Y152	Y152	Y137	Y170	Y169	Y170	Y171
	M254	M300	-	-	-	-	-	-	-	-
	-	-	M75	M57	M57	M78	M75	M75	M75	M76
35	-	-	M477	-						
				M328						
	-	M313	-	-						

W507,

wherein

CcL: *Coprinus cinereus* laccase comprising the amino acid sequence shown in SEQ ID No. 1;

5 PpL1: *Polyporus pinsitus* (I) laccase comprising the amino acid sequence shown in SEQ ID No. 2;

PpL2: *Polyporus pinsitus* (II) laccase comprising the amino acid sequence shown in SEQ ID No. 3;

PrL: *Phlebia radiata* laccase comprising the amino acid sequence
10 shown in SEQ ID No. 4;

RSL3: *Rhizoctonia solani* (I) laccase comprising the amino acid sequence shown in SEQ ID No. 5;

RSL2: *Rhizoctonia solani* (II) laccase comprising the amino acid sequence shown in SEQ ID No. 6;

15 RSL4: *Rhizoctonia solani* (III) laccase comprising the amino acid sequence shown in SEQ ID No. 7;

RSL1: *Rhizoctonia solani* (IV) laccase comprising the amino acid sequence shown in SEQ ID No. 8;

StL: *Scytalidium thermophilum* laccase comprising the amino acid
20 sequence shown in SEQ ID No. 9; and

MtL: *Myceliophthora thermophila* laccase comprising the amino acid sequence shown in SEQ ID No. 10.

The above shown rows have homologous positions. (-) or () =
25 not present in this laccase.

The following variants are preferred:

A variant of a parent *Coprinus* laccase, which comprises one
30 or more of the following substitutions in SEQ ID No. 1:

W125 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
Y134 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y126 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y170 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
35 M75 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H;
M477 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

In particular a variant of a parent *Coprinus laccase*, which comprises one or more of the following substitutions in SEQ ID No. 1:

5 W125 F, H;
Y134 F;
Y126 F;
Y170 F;
M75 F, V, I, L, Q;
10 M477 F, V, I, L, Q.

A variant of a parent *Polyporus pinsitus (I)* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:

15 W107 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
Y116 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y108 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y152 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
M57 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H;
20 M328 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

In particular a variant of a parent *Polyporus pinsitus (I)* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:

25 W107 F, H;
Y116 F;
Y108 F;
Y152 F;
M57 F, V, I, L, Q;
30 M328 F, V, I, L, Q.

A variant of a parent *Polyporus pinsitus (II)* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 3:

35 W107 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
Y116 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y108 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

Y152 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
M57 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

In particular a variant of a parent *Polyporus pinsitus* (II) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 3:

W107 F, H;
Y116 F;
Y108 F;
10 Y152 F;
M57 F, V, I, L, Q.

A variant of a parent *Phlebia radiata* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 4:

W128 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
Y137 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y129 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y137 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
20 M78 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

In particular a variant of a parent *Phlebia radiata* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 4:

25 W128 F, H;
Y137 F;
Y129 F;
Y137 F;
M78 F, V, I, L, Q.

30

A variant of a parent *Rhizoctonia solani* (I) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 5:

W126 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
35 Y135 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y127 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y171 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

M76 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

In particular a variant of a parent *Rhizoctonia solani* (I) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 5:

W126 F, H;

Y135 F;

Y127 F;

Y171 F;

10 M76 F, V, I, L, Q.

A variant of a parent *Rhizoctonia solani* (II) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 6:

15 W439 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;

W125 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;

Y134 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

Y126 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

Y170 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

20 M75 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

In particular a variant of a parent *Rhizoctonia solani* (II) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 6:

25 W439 F, H;

W125 F, H;

Y134 F;

Y126 F;

Y170 F;

30 M75 F, V, I, L, Q.

A variant of a parent *Rhizoctonia solani* (III) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 7:

35 W411 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;

W125 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;

Y134 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

Y126 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
Y170 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
M75 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

- 5 In particular a variant of a parent *Rhizoctonia solani* (III) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 7:

W411 F, H;

W125 F, H;

- 10 Y134 F;

Y126 F;

Y170 F;

M75 F, V, I, L, Q.

- 15 A variant of a parent *Rhizoctonia solani* (IV) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 8:

W411 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;

W125 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;

- 20 Y134 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

Y126 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

Y170 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;

M75 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

- 25 In particular a variant of a parent *Rhizoctonia solani* (IV) laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 8:

W411 F, H;

W125 F, H;

- 30 Y134 F;

Y126 F;

Y170 F;

M75 F, V, I, L, Q.

- 35 A variant of a parent *Scytalidium thermophilum* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 9:

M483 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H;
 W422 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
 W181 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
 Y190 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
 5 M530 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H;
 Y182 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
 Y221 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
 M300 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H;
 M313 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

10

In particular a variant of a parent *Scytalidium thermophilum* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 9:

M483 F, V, I, L, Q;
 15 W422 F, H;
 W181 F, H;
 Y190 F;
 M530 F, V, I, L, Q;
 Y182 F;
 20 Y221 F;
 M300 F, V, I, L, Q;
 M313 F, V, I, L, Q.

A variant of a parent *Myceliophthora thermophila* laccase,
 25 which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:

M433 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H;
 W373 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
 W136 A, V, L, I, P, F, M, G, S, T, C, Y, N, Q, D, E, K, R, H;
 30 Y145 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
 M480 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H;
 Y137 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
 Y176 A, V, L, I, P, F, W, G, S, T, C, M, N, Q, D, E, K, R, H;
 M254 A, V, L, I, P, F, W, G, S, T, C, Y, N, Q, D, E, K, R, H.

35

In particular a variant of a parent *Myceliophthora thermophila* laccase, which comprises a mutation in a position

corresponding to at least one of the following positions in SEQ ID No. 10:

M433 F, V, I, L, Q;

W373 F, H;

5 W136 F, H;

Y145 F;

M480 F, V, I, L, Q;

Y137 F;

Y176 F;

10 M254 F, V, I, L, Q.

Methods of preparing laccase variants

Several methods for introducing mutations into genes are known in the art. After a brief discussion of the cloning of
15 laccase-encoding DNA sequences, methods for generating mutations at specific sites within the laccase-encoding sequence will be discussed.

Cloning a DNA sequence encoding a laccase

The DNA sequence encoding a parent laccase may be isolated
20 from any cell or microorganism producing the laccase in question, using various methods well known in the art. First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the laccase to be studied. Then, if the amino acid sequence of the laccase is
25 known, homologous, labelled oligonucleotide probes may be synthesized and used to identify laccase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labelled oligonucleotide probe containing sequences homologous to a known laccase gene could be used as a probe to
30 identify laccase-encoding clones, using hybridization and washing conditions of lower stringency.

A method for identifying laccase-encoding clones involves inserting cDNA into an expression vector, such as a plasmid, transforming laccase-negative fungi with the resulting cDNA
35 library, and then plating the transformed fungi onto agar containing a substrate for laccase, thereby allowing clones expressing the laccase to be identified.

Alternatively, the DNA sequence encoding the enzyme may be

prepared synthetically by established standard methods, e.g. the phosphoroamidite method. In the phosphoroamidite method, oligonucleotides are synthesized, e.g. in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

5 Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating fragments of synthetic, genomic or cDNA origin (as appropriate, the fragments corresponding to various parts of the entire DNA sequence), in accordance with
10 standard techniques. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers.

Site-directed mutagenesis

Once a laccase-encoding DNA sequence has been isolated, and
15 desirable sites for mutation identified, mutations may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired mutation sites; mutant nucleotides are inserted during oligonucleotide synthesis. In a specific method, a single-stranded gap of DNA, bridging the
20 laccase-encoding sequence, is created in a vector carrying the laccase gene. Then the synthetic nucleotide, bearing the desired mutation, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is then filled in with T7 DNA polymerase and the construct is ligated using T4 ligase. A
25 specific example of this method is described in Morinaga et al. (1984). US 4,760,025 discloses the introduction of oligonucleotides encoding multiple mutations by performing minor alterations of the cassette. However, an even greater variety of mutations can be introduced at any one time by the Morinaga method, because
30 a multitude of oligonucleotides, of various lengths, can be introduced.

Another method of introducing mutations into laccase-encoding DNA sequences is described in Nelson and Long (1989). It involves the 3-step generation of a PCR fragment containing the desired
35 mutation introduced by using a chemically synthesized DNA strand as one of the primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the mutation may be isolated by cleavage with restriction endonucleases and

reinserted into an expression plasmid.

Random mutagenesis

The random mutagenesis of a DNA sequence encoding a parent
5 laccase may conveniently be performed by use of any method known
in the art.

For instance, the random mutagenesis may be performed by use
of a suitable physical or chemical mutagenizing agent, by use of
a suitable oligonucleotide, or by subjecting the DNA sequence to
10 PCR generated mutagenesis. Furthermore, the random mutagenesis
may be performed by use of any combination of these mutagenizing
agents.

The mutagenizing agent may, e.g., be one which induces tran-
sitions, transversions, inversions, scrambling, deletions, and/or
15 insertions.

Examples of a physical or chemical mutagenizing agent
suitable for the present purpose include ultraviolet (UV) ir-
radiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine
(MNNG), O-methyl hydroxylamine, nitrous acid, ethyl methane
20 sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide
analogues.

When such agents are used, the mutagenesis is typically per-
formed by incubating the DNA sequence encoding the parent enzyme
to be mutagenized in the presence of the mutagenizing agent of
25 choice under suitable conditions for the mutagenesis to take
place, and selecting for mutated DNA having the desired
properties.

When the mutagenesis is performed by the use of an oligo-
nucleotide, the oligonucleotide may be doped or spiked with the
30 three non-parent nucleotides during the synthesis of the
oligonucleotide at the positions which are to be changed. The
doping or spiking may be done so that codons for unwanted amino
acids are avoided. The doped or spiked oligonucleotide can be
incorporated into the DNA encoding the laccase enzyme by any
35 published technique, using e.g. PCR, LCR or any DNA polymerase
and ligase.

When PCR-generated mutagenesis is used, either a chemically
treated or non-treated gene encoding a parent laccase enzyme is

subjected to PCR under conditions that increase the mis-incorporation of nucleotides (Deshler 1992; Leung et al., Technique, Vol.1, 1989, pp. 11-15).

A mutator strain of *E. coli* (Fowler et al., Molec. Gen. 5 Genet., 133, 1974, pp. 179-191), *S. cerevisiae* or any other microbial organism may be used for the random mutagenesis of the DNA encoding the laccase enzyme by e.g. transforming a plasmid containing the parent enzyme into the mutator strain, growing the mutator strain with the plasmid and isolating the mutated plasmid 10 from the mutator strain. The mutated plasmid may subsequently be transformed into the expression organism.

The DNA sequence to be mutagenized may conveniently be present in a genomic or cDNA library prepared from an organism expressing the parent laccase enzyme. Alternatively, the DNA se- 15 quence may be present on a suitable vector such as a plasmid or a bacteriophage, which as such may be incubated with or otherwise exposed to the mutagenizing agent. The DNA to be mutagenized may also be present in a host cell either by being integrated in the genome of said cell or by being present on a vector harboured in 20 the cell. Finally, the DNA to be mutagenized may be in isolated form. It will be understood that the DNA sequence to be subjected to random mutagenesis is preferably a cDNA or a genomic DNA sequence.

In some cases it may be convenient to amplify the mutated DNA 25 sequence prior to the expression step or the screening step being performed. Such amplification may be performed in accordance with methods known in the art, the presently preferred method being PCR-generated amplification using oligonucleotide primers prepared on the basis of the DNA or amino acid sequence of the 30 parent enzyme.

Subsequent to the incubation with or exposure to the mutagenizing agent, the mutated DNA is expressed by culturing a suitable host cell carrying the DNA sequence under conditions allowing expression to take place. The host cell used for this 35 purpose may be one which has been transformed with the mutated DNA sequence, optionally present on a vector, or one which was carried the DNA sequence encoding the parent enzyme during the mutagenesis treatment. Examples of suitable host cells are fungal

hosts such as *Aspergillus niger* or *Aspergillus oryzae*.

The mutated DNA sequence may further comprise a DNA sequence encoding functions permitting expression of the mutated DNA sequence.

Localized random mutagenesis

The random mutagenesis may advantageously be localized to a part of the parent laccase in question. This may, e.g., be advantageous when certain regions of the enzyme have been identified to be of particular importance for a given property of the enzyme, and when modified are expected to result in a variant having improved properties. Such regions may normally be identified when the tertiary structure of the parent enzyme has been elucidated and related to the function of the enzyme.

The localized random mutagenesis is conveniently performed by use of PCR-generated mutagenesis techniques as described above or any other suitable technique known in the art.

Alternatively, the DNA sequence encoding the part of the DNA sequence to be modified may be isolated, e.g. by being inserted into a suitable vector, and said part may subsequently be subjected to mutagenesis by use of any of the mutagenesis methods discussed above.

With respect to the screening step in the above-mentioned method of the invention, this may conveniently be performed by use of aa filter assay based on the following principle:

A microorganism capable of expressing the mutated laccase enzyme of interest is incubated on a suitable medium and under suitable conditions for the enzyme to be secreted, the medium being provided with a double filter comprising a first protein-binding filter and on top of that a second filter exhibiting a low protein binding capability. The microorganism is located on the second filter. Subsequent to the incubation, the first filter comprising enzymes secreted from the microorganisms is separated from the second filter comprising the microorganisms. The first filter is subjected to screening for the desired enzymatic activity and the corresponding microbial colonies present on the second filter are identified.

The filter used for binding the enzymatic activity may be any protein binding filter e.g. nylon or nitrocellulose. The top filter carrying the colonies of the expression organism may be any filter that has no or low affinity for binding proteins e.g. 5 cellulose acetate or Durapore™. The filter may be pretreated with any of the conditions to be used for screening or may be treated during the detection of enzymatic activity.

The enzymatic activity may be detected by a dye, fluorescence, precipitation, pH indicator, IR-absorbance or any 10 other known technique for detection of enzymatic activity.

The detecting compound may be immobilized by any immobilizing agent, e.g., agarose, agar, gelatine, polyacrylamide, starch, filter paper, cloth; or any combination of immobilizing agents.

15 Testing of variants of the invention

The storage stability of *Coprinus* variants or *Coprinus*-like variants should be investigated at 40°C for 2 weeks at pH 5, 8 and 9.3, respectively. The stability of the parent laccase and the variants may be tested both in a liquid buffer formulation 20 and in a lyophilized form.

According to the invention the residual activity of the variants following two weeks of incubation are then compared to the residual activity of the parent laccase, and variants with an improved stability at either pH 5, 8 or 9.3 are selected.

25

Laccase activity

In the context of this invention, the laccase activity was measured using 10-(2-hydroxyethyl)-phenoxazine (HEPO) as substrate for the various laccases. HEPO was synthesized using 30 the same procedure as described for 10-(2-hydroxyethyl)-phenothiazine, (G. Cauquil in Bulletin de la Society Chimique de France, 1960, p. 1049). In the presence of oxygen laccases (E.C. 1.10.3.2) oxidize HEPO to a HEPO radical that can be monitored photometrically at 528 nm.

35 The *Coprinus cinereus* laccase was measured using 0.4 mM HEPO in 50 mM sodium acetate, pH 5.0, 0.05% TWEEN-20 at 30°C. The absorbance at 528 nm was followed for 200 s and the rate calculated from the linear part of the progress curve.

The *Myceliophthora thermophila* laccase was measured using 0.4 mM HEPO in 25 mM Tris-HCl, pH 7.5, 0.05% Tween-20 at 30 °C. The absorbance at 528 nm was followed for 200 s and the rate calculated from the linear part of the progress curve.

5 The *Polyporus pinsitus* laccase was measured using 0.4 mM HEPO in 50 mM MES-NaOH, pH 5.5. The absorbance at 528 nm was followed for 200 s and the rate calculated from the linear part of the progress curve.

10 Expression of laccase variants

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in enzyme form, using an expression vector which typically includes control
15 sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

The recombinant expression vector carrying the DNA sequence encoding a laccase variant of the invention may be any vector
20 which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is
25 independent of chromosomal replication, e.g. a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an artificial chromosome. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s)
30 into which it has been integrated.

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either
35 homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding a laccase variant of the invention, especially in a fungal host, are those derived from the gene encoding *A. oryzae*

TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α -amylase, *A. niger* acid stable α -amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

5 The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the laccase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same
10 sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

15 The vector may also comprise a selectable marker, e.g. a gene, the product of which complements a defect in the host cell, such as one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracyclin resistance. Furthermore, the vector may comprise *Aspergillus* selection markers
20 such as *amdS*, *argB*, *niaD* and *sC*, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, e.g. as described in WO 91/17243.

The procedures used to ligate the DNA construct of the invention encoding a laccase variant, the promoter, terminator and
25 other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al. (1989)).

The cell of the invention, either comprising a DNA construct
30 or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of a laccase variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or
35 more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of

the DNA constructs into the host chromosome may be performed according to conventional methods, e.g. by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g. a fungal cell.

The filamentous fungus may advantageously belong to a species of *Aspergillus*, e.g. *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known per se. A suitable procedure for transformation of *Aspergillus* host cells is described in EP 238 023.

In a yet further aspect, the present invention relates to a method of producing a laccase variant of the invention, which method comprises cultivating a host cell as described above under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the laccase variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. as described in catalogues of the American Type Culture Collection).

The laccase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

35

Industrial Applications

The laccase variants of this invention possesses valuable properties allowing for various industrial applications, in

particular lignin modification, paper strengthening, dye transfer inhibition in detergents, phenol polymerization, hair dyeing, bleaching of textiles (in particular bleaching of denim as described in WO 96/12845 and WO 96/12846) and waste water treatment. Any detergent composition normally used for enzymes may be used, e.g., the detergent compositions disclosed in WO 95/01426.

The invention is further illustrated in the following examples, which are not intended to be in any way limiting to the scope of the invention as claimed.

EXAMPLE 1

Storage stability of the wild type *Myceliophthora thermophila* and the *Polyporus pinsitus* laccases.

The storage stability of the *Myceliophthora thermophila* and the *Polyporus pinsitus* laccases was tested for 2 weeks at 40°C at pH 5, 8 and 9.3, respectively.

The laccase (1 mg/ml) was dialyzed against 0.1 M sodium acetate, pH 5, or 0.1 M Tris-maleate, pH 8, or 0.1 M Tris-maleate, pH 9.3. Following dialysis the different preparations were poured into two sets of glass vials with screw caps: one for the liquid formulation and the other one for the lyophilized form. After two weeks of incubation the enzyme activity was measured as described above and the residual activity of the enzymes was calculated in percentage using a preparation of *Myceliophthora thermophila* and *Polyporus pinsitus* kept at 4°C as references. The results are given below in Table 1 and 2.

30

Table 1 Storage stability of *Myceliophthora thermophila*

pH	Liquid formulation		Lyophilized form	
	Residual (%)	activity	Residual (%)	activity
5.0	<5		<5	
8.0	<5		<5	
9.3	35		30	

Table 2 Storage stability of *Polyporus pinsitus*

pH	Liquid formulation		Lyophilized form	
	Residual (%)	activity	Residual (%)	activity
5.0	<5		n.d.	
8.0	35		n.d.	
9.3	n.d.*		n.d.	

* not determined

5 EXAMPLE 2

Homology building of the *Polyporus pinsitus* 3D-structure

Using sequence homology of *Coprinus cinereus* (CcL) to other sequences, e.g., *Polyporus pinsitus*, *Coprinus*-like 3 D-structures
10 can be found.

In comparison with the *Coprinus cinereus*, used for elucidating the structure, *Polyporus pinsitus* differs in a number of residues. The model may be built using the HOMOLOGY program from BIOSYM. The program substitutes the amino acids in the
15 *Coprinus cinereus* with amino acids from *Polyporus pinsitus* in the homologous positions defined in the program as structurally conserved regions (SCR). The residues in between are built using the LOOP option with GENERATE. Using these steps a crude model may be obtained which gives information of spatial interactions.

20 The structure can be refined using the method described in the HOMOLOGY package.

EXAMPLE 3

25 Storage stability of *Myceliophthora thermophila* variants

Laccase activity:

In this Example the *Myceliophthora thermophila* laccase variants were measured using 0.4 mM HEPO in 0.1 M Tris-maleate,
30 pH 7.5, 0.05% TWEEN-20 at 30°C. The absorbance at 528 nm was followed for 200 s and the rate calculated from the linear part

of the progress curve.

The storage stability of the *Myceliophthora thermophila* variants were tested for 4 weeks at 40°C at pH 5, 7, and 9.3, respectively. The laccase (1 mg/ml) was dialyzed against 0.1 M Tris-maleate, pH 5 or 0.1 M Tris-maleate, pH 7 or 0.1 M Tris-maleate, pH 9.3. Following dialysis the different preparations were poured into two set of glass vials with screw caps: one for the liquid formulation and the other set of glasses for lyophilization. Following two and four weeks of incubation the enzyme activity was measured as described above and the residual activity of the variants were calculated in percentage using a preparation kept at 4°C as reference.

Table 3. Storage stability of *Myceliophthora thermophila* variants, lyophilized formulation

	Residual activity, pH 5		Residual activity, pH 7		Residual activity, pH 9.2	
	2 weeks	4 weeks	2 weeks	4 weeks	2 weeks	4 weeks
wt	18	18	55	36	59	38
W136F	<5	<5	76	64	88	77
Y137F	12	<5	58	41	64	49
Y145F	<5	<5	53	20	45	51
W373F	14	14	33	19	51	36
M433I	7	<5	57	43	74	35
M480L	33	18	65	32	72	52
W507F	18	<5	72	51	68	71

In lyophilized form none of the tested variants have improved stability at pH 5. At pH 7 and pH 9.2 both W136F and W507F have increased stability. At pH 9.2 M480L is also better than wt.

Table 4. Storage stability of *Myceliophthora thermophila* variants, liquid formulation

	Residual activity, 5, 2 weeks	pH	Residual activity, pH 7, 2 weeks	Residual activity, pH 9.2, 2 weeks
wt	<5		5	20
W136F	5		28	55
Y137F	<5		<5	<5
Y145F	<5		<5	<5
W373F	<5		40	<5
M433I	8		40	65
M480L	<5		<5	15
W507F	<5		<5	22

- Also in the liquid formulation none of the tested variants
- 5 have improved stability at pH 5. At pH 7 and pH 9.2 both W136F and M433I has increased stability. At pH7 W373F has better stability than wt but the variant loses the stability completely at pH 9.2.
- 10 Of the tested variants only W136F has increased stability in both formulations.

Appendix 1:

SEQRES 1 A 504 GLN ILE VAL ASN SER VAL ASP THR MET THR LEU THR ASN
SEQRES 2 A 504 ALA ASN VAL SER PRO ASP GLY PHE THR ARG ALA GLY ILE
5 SEQRES 3 A 504 LEU VAL ASN GLY VAL HIS GLY PRO LEU ILE ARG GLY GLY
SEQRES 4 A 504 LYS ASN ASP ASN PHE GLU LEU ASN VAL VAL ASN ASP LEU
SEQRES 5 A 504 ASP ASN PRO THR MET LEU ARG PRO THR SER ILE HIS TRP
SEQRES 6 A 504 HIS GLY LEU PHE GLN ARG GLY THR ASN TRP ALA ASN GLY
SEQRES 7 A 504 ALA ASP GLY VAL ASN GLN CYS PRO ILE SER PRO GLY HIS
10 SEQRES 8 A 504 ALA PHE LEU TYR LYS PHE THR PRO ALA GLY HIS ALA GLY
SEQRES 9 A 504 THR PHE TRP TYR HIS SER HIS PHE GLY THR GLN TYR CYS
SEQRES 10 A 504 ASP GLY LEU ARG GLY PRO MET VAL ILE TYR ASP ASP ASN
SEQRES 11 A 504 ASP PRO HIS ALA ALA LEU TYR ASP GLU ASP ASP GLU ASN
SEQRES 12 A 504 THR ILE ILE THR LEU ALA ASP TRP TYR HIS ILE PRO ALA
15 SEQRES 13 A 504 PRO SER ILE GLN GLY ALA ALA GLN PRO ASP ALA THR LEU
SEQRES 14 A 504 ILE ASN GLY LYS GLY ARG TYR VAL GLY GLY PRO ALA ALA
SEQRES 15 A 504 GLU LEU SER ILE VAL ASN VAL GLU GLN GLY LYS LYS TYR
SEQRES 16 A 504 ARG MET ARG LEU ILE SER LEU SER CYS ASP PRO ASN TRP
SEQRES 17 A 504 GLN PHE SER ILE ASP GLY HIS GLU LEU THR ILE ILE GLU
20 SEQRES 18 A 504 VAL ASP GLY ASN LEU THR GLU PRO HIS THR VAL ASP ARG
SEQRES 19 A 504 LEU GLN ILE PHE THR GLY GLN ARG TYR SER PHE VAL LEU
SEQRES 20 A 504 ASP ALA ASN GLN PRO VAL ASP ASN TYR TRP ILE ARG ALA
SEQRES 21 A 504 GLN PRO ASN LYS GLY ARG ASN GLY LEU ALA GLY THR PHE
SEQRES 22 A 504 ALA ASN GLY VAL ASN SER ALA ILE LEU ARG TYR ALA GLY
25 SEQRES 23 A 504 ALA ALA ASN ALA ASP PRO THR THR SER ALA ASN PRO ASN
SEQRES 24 A 504 PRO ALA GLN LEU ASN GLU ALA ASP LEU HIS ALA LEU ILE
SEQRES 25 A 504 ASP PRO ALA ALA PRO GLY ILE PRO THR PRO GLY ALA ALA
SEQRES 26 A 504 ASN VAL ASN LEU ARG PHE GLN LEU GLY PHE SER GLY GLY
SEQRES 27 A 504 ARG PHE THR ILE ASN GLY THR ALA TYR GLU SER PRO SER
30 SEQRES 28 A 504 VAL PRO THR LEU LEU GLN ILE MET SER GLY ALA GLN SER
SEQRES 29 A 504 ALA ASN ASP LEU LEU PRO ALA GLY SER VAL TYR GLU LEU
SEQRES 30 A 504 PRO ARG ASN GLN VAL VAL GLU LEU VAL VAL PRO ALA GLY
SEQRES 31 A 504 VAL LEU GLY GLY PRO HIS PRO PHE HIS LEU HIS GLY HIS
SEQRES 32 A 504 ALA PHE SER VAL VAL ARG SER ALA GLY SER SER THR TYR
35 SEQRES 33 A 504 ASN PHE VAL ASN PRO VAL LYS ARG ASP VAL VAL SER LEU
SEQRES 34 A 504 GLY VAL THR GLY ASP GLU VAL THR ILE ARG PHE VAL THR
SEQRES 35 A 504 ASP ASN PRO GLY PRO TRP PHE PHE HIS CYS HIS ILE GLU
SEQRES 36 A 504 PHE HIS LEU MET ASN GLY LEU ALA ILE VAL PHE ALA GLU

SEQRES 37 A 504 ASP MET ALA ASN THR VAL ASP ALA ASN ASN PRO PRO VAL
SEQRES 38 A 504 GLU TRP ALA GLN LEU CYS GLU ILE TYR ASP ASP LEU PRO
SEQRES 39 A 504 PRO GLU ALA THR SER ILE GLN THR VAL VAL
SSBOND 1 CYS 85 CYS 487
5 SSBOND 2 CYS 117 CYS 204
CRYST 45.390 85.720 143.070 90.00 90.00 90.00 P212121
SCALE1 0.02203 0.00000 0.00000 0.00000
SCALE2 0.00000 0.01167 0.00000 0.00000
SCALE3 0.00000 0.00000 0.00699 0.00000
10 ATOM 1 N ALA A 1 0 18.748 34.495 5.326 1.00 36.36
ATOM 2 CA ALA A 1 0 19.554 35.757 5.185 1.00 35.87
ATOM 3 C ALA A 1 0 19.785 36.380 6.558 1.00 34.53
ATOM 4 O ALA A 1 0 19.248 35.884 7.577 1.00 35.40
ATOM 5 CB ALA A 1 0 19.050 36.675 4.107 1.00 36.65
15 ATOM 6 N ILE A 2 0 20.844 37.201 6.659 1.00 31.00
ATOM 7 CA ILE A 2 0 21.310 37.654 7.963 1.00 27.71
ATOM 8 C ILE A 2 0 21.368 39.165 8.117 1.00 25.19
ATOM 9 O ILE A 2 0 21.789 39.861 7.192 1.00 23.77
ATOM 10 CB ILE A 2 0 22.744 37.107 8.206 1.00 28.28
20 ATOM 11 CG1 ILE A 2 0 22.790 35.590 8.022 1.00 28.54
ATOM 12 CG2 ILE A 2 0 23.285 37.557 9.554 1.00 27.91
ATOM 13 CD1 ILE A 2 0 23.334 34.738 9.130 1.00 29.32
ATOM 14 N VAL A 3 0 20.986 39.659 9.283 1.00 22.31
ATOM 15 CA VAL A 3 0 21.093 41.092 9.540 1.00 22.78
25 ATOM 16 C VAL A 3 0 22.246 41.297 10.524 1.00 22.62
ATOM 17 O VAL A 3 0 22.460 40.556 11.467 1.00 21.74
ATOM 18 CB VAL A 3 0 19.801 41.849 9.799 1.00 23.54
ATOM 19 CG1 VAL A 3 0 18.537 40.985 9.684 1.00 21.30
ATOM 20 CG2 VAL A 3 0 19.760 42.709 11.055 1.00 21.32
30 ATOM 21 N ASN A 4 0 23.122 42.261 10.209 1.00 23.39
ATOM 22 CA ASN A 4 0 24.303 42.520 11.021 1.00 23.45
ATOM 23 C ASN A 4 0 24.002 43.517 12.126 1.00 24.44
ATOM 24 O ASN A 4 0 22.928 44.122 12.160 1.00 23.05
ATOM 25 CB ASN A 4 0 25.477 42.965 10.149 1.00 24.77
35 ATOM 26 CG ASN A 4 0 25.726 41.991 9.021 1.00 26.62
ATOM 27 OD1 ASN A 4 0 25.668 42.388 7.849 1.00 30.29
ATOM 28 ND2 ASN A 4 0 25.923 40.719 9.324 1.00 27.59
ATOM 29 N SER A 5 0 24.960 43.707 13.040 1.00 24.28

	ATOM	30	CA	SER A	5	0	24.702	44.636	14.143	1.00	25.77
	ATOM	31	C	SER A	5	0	24.595	46.090	13.701	1.00	24.41
	ATOM	32	O	SER A	5	0	23.973	46.862	14.452	1.00	23.55
	ATOM	33	CB	SER A	5	0	25.741	44.405	15.240	1.00	26.18
5	ATOM	34	OG	SER A	5	0	26.976	44.750	14.641	1.00	27.89
	ATOM	35	N	VAL A	6	0	25.104	46.517	12.539	1.00	24.01
	ATOM	36	CA	VAL A	6	0	24.770	47.863	12.096	1.00	25.06
	ATOM	37	C	VAL A	6	0	24.131	47.617	10.731	1.00	25.57
	ATOM	38	O	VAL A	6	0	24.778	47.030	9.874	1.00	28.07
10	ATOM	39	CB	VAL A	6	0	25.722	49.032	12.155	1.00	26.65
	ATOM	40	CG1	VAL A	6	0	26.937	48.759	13.025	1.00	26.73
	ATOM	41	CG2	VAL A	6	0	26.098	49.614	10.801	1.00	25.50
	ATOM	42	N	ASP A	7	0	22.848	47.952	10.605	1.00	23.82
	ATOM	43	CA	ASP A	7	0	22.173	47.543	9.369	1.00	24.07
15	ATOM	44	C	ASP A	7	0	20.794	48.170	9.276	1.00	23.66
	ATOM	45	O	ASP A	7	0	20.342	48.845	10.204	1.00	23.47
	ATOM	46	CB	ASP A	7	0	21.996	46.012	9.444	1.00	23.43
	ATOM	47	CG	ASP A	7	0	22.017	45.317	8.111	1.00	23.78
	ATOM	48	OD1	ASP A	7	0	21.805	45.937	7.055	1.00	23.74
20	ATOM	49	OD2	ASP A	7	0	22.255	44.089	8.099	1.00	24.62
	ATOM	50	N	THR A	8	0	20.155	47.881	8.158	1.00	23.88
	ATOM	51	CA	THR A	8	0	18.799	48.359	7.928	1.00	24.45
	ATOM	52	C	THR A	8	0	17.813	47.189	7.950	1.00	22.49
	ATOM	53	O	THR A	8	0	18.143	46.142	7.377	1.00	22.56
25	ATOM	54	CB	THR A	8	0	18.694	49.108	6.579	1.00	25.75
	ATOM	55	OG1	THR A	8	0	19.573	50.242	6.719	1.00	28.53
	ATOM	56	CG2	THR A	8	0	17.295	49.656	6.339	1.00	25.55
	ATOM	57	N	MET A	9	0	16.677	47.364	8.602	1.00	19.10
	ATOM	58	CA	MET A	9	0	15.650	46.311	8.616	1.00	20.47
30	ATOM	59	C	MET A	9	0	14.392	46.863	7.925	1.00	21.97
	ATOM	60	O	MET A	9	0	13.638	47.638	8.544	1.00	19.49
	ATOM	61	CB	MET A	9	0	15.308	45.871	10.022	1.00	20.49
	ATOM	62	CG	MET A	9	0	16.351	44.982	10.682	1.00	22.11
	ATOM	63	SD	MET A	9	0	16.192	44.917	12.482	1.00	24.71
35	ATOM	64	CE	MET A	9	0	14.640	44.024	12.635	1.00	22.61
	ATOM	65	N	THR A	10	0	14.246	46.516	6.641	1.00	21.81
	ATOM	66	CA	THR A	10	0	13.073	47.064	5.926	1.00	23.43
	ATOM	67	C	THR A	10	0	11.912	46.081	6.046	1.00	22.90

	ATOM	68	O	THR	A	10	0	12.056	44.890	5.719	1.00	23.55
	ATOM	69	CB	THR	A	10	0	13.390	47.384	4.459	1.00	24.69
	ATOM	70	OG1	THR	A	10	0	14.533	48.261	4.456	1.00	26.08
	ATOM	71	CG2	THR	A	10	0	12.216	48.028	3.742	1.00	23.95
5	ATOM	72	N	LEU	A	11	0	10.820	46.600	6.583	1.00	21.13
	ATOM	73	CA	LEU	A	11	0	9.615	45.836	6.846	1.00	21.10
	ATOM	74	C	LEU	A	11	0	8.607	45.957	5.709	1.00	24.58
	ATOM	75	O	LEU	A	11	0	8.124	47.056	5.358	1.00	23.89
	ATOM	76	CB	LEU	A	11	0	9.045	46.411	8.129	1.00	21.29
10	ATOM	77	CG	LEU	A	11	0	9.474	45.955	9.508	1.00	22.26
	ATOM	78	CD1	LEU	A	11	0	10.952	45.742	9.692	1.00	22.42
	ATOM	79	CD2	LEU	A	11	0	8.978	46.931	10.583	1.00	22.75
	ATOM	80	N	THR	A	12	0	8.272	44.836	5.057	1.00	24.01
	ATOM	81	CA	THR	A	12	0	7.302	44.851	3.980	1.00	24.33
15	ATOM	82	C	THR	A	12	0	6.322	43.677	4.123	1.00	25.34
	ATOM	83	O	THR	A	12	0	6.480	42.740	4.913	1.00	25.62
	ATOM	84	CB	THR	A	12	0	7.882	44.776	2.560	1.00	25.12
	ATOM	85	OG1	THR	A	12	0	8.575	43.548	2.377	1.00	24.05
	ATOM	86	CG2	THR	A	12	0	8.847	45.905	2.217	1.00	25.26
20	ATOM	87	N	ASN	A	13	0	5.261	43.760	3.335	1.00	24.09
	ATOM	88	CA	ASN	A	13	0	4.232	42.722	3.299	1.00	22.87
	ATOM	89	C	ASN	A	13	0	4.422	41.954	1.989	1.00	22.13
	ATOM	90	O	ASN	A	13	0	4.809	42.600	1.023	1.00	22.32
	ATOM	91	CB	ASN	A	13	0	2.852	43.355	3.311	1.00	21.58
25	ATOM	92	CG	ASN	A	13	0	2.526	44.060	4.607	1.00	22.50
	ATOM	93	OD1	ASN	A	13	0	2.187	45.245	4.648	1.00	22.20
	ATOM	94	ND2	ASN	A	13	0	2.615	43.306	5.705	1.00	21.81
	ATOM	95	N	ALA	A	14	0	4.218	40.655	1.985	1.00	21.00
	ATOM	96	CA	ALA	A	14	0	4.270	39.869	0.762	1.00	21.93
30	ATOM	97	C	ALA	A	14	0	3.571	38.533	1.078	1.00	20.77
	ATOM	98	O	ALA	A	14	0	3.292	38.309	2.259	1.00	20.45
	ATOM	99	CB	ALA	A	14	0	5.676	39.618	0.248	1.00	23.72
	ATOM	100	N	ASN	A	15	0	3.366	37.695	0.072	1.00	18.88
	ATOM	101	CA	ASN	A	15	0	2.748	36.412	0.337	1.00	19.67
35	ATOM	102	C	ASN	A	15	0	3.798	35.457	0.873	1.00	19.19
	ATOM	103	O	ASN	A	15	0	4.891	35.474	0.338	1.00	19.57
	ATOM	104	CB	ASN	A	15	0	2.114	35.721	-0.875	1.00	21.13
	ATOM	105	CG	ASN	A	15	0	0.839	36.457	-1.284	1.00	21.15

	ATOM	106	OD1	ASN	A	15	0	0.343	37.207	-0.472	1.00	20.87
	ATOM	107	ND2	ASN	A	15	0	0.379	36.284	-2.501	1.00	20.00
	ATOM	108	N	VAL	A	16	0	3.358	34.614	1.772	1.00	19.11
	ATOM	109	CA	VAL	A	16	0	4.322	33.628	2.342	1.00	18.90
5	ATOM	110	C	VAL	A	16	0	3.626	32.293	2.345	1.00	19.25
	ATOM	111	O	VAL	A	16	0	2.386	32.281	2.406	1.00	16.71
	ATOM	112	CB	VAL	A	16	0	4.612	34.317	3.691	1.00	19.95
	ATOM	113	CG1	VAL	A	16	0	3.990	33.749	4.937	1.00	18.58
	ATOM	114	CG2	VAL	A	16	0	6.091	34.603	3.814	1.00	21.38
10	ATOM	115	N	SER	A	17	0	4.312	31.157	2.303	1.00	18.57
	ATOM	116	CA	SER	A	17	0	3.678	29.869	2.410	1.00	20.90
	ATOM	117	C	SER	A	17	0	4.608	28.866	3.065	1.00	21.12
	ATOM	118	O	SER	A	17	0	5.106	27.939	2.448	1.00	21.24
	ATOM	119	CB	SER	A	17	0	3.186	29.285	1.080	1.00	23.95
15	ATOM	120	OG	SER	A	17	0	4.204	29.399	0.125	1.00	26.79
	ATOM	121	N	PRO	A	18	0	4.834	29.051	4.358	1.00	20.78
	ATOM	122	CA	PRO	A	18	0	5.703	28.216	5.141	1.00	20.02
	ATOM	123	C	PRO	A	18	0	5.197	26.793	5.376	1.00	19.74
	ATOM	124	O	PRO	A	18	0	5.978	25.920	5.753	1.00	17.97
20	ATOM	125	CB	PRO	A	18	0	5.889	28.954	6.481	1.00	19.27
	ATOM	126	CG	PRO	A	18	0	4.701	29.832	6.536	1.00	21.41
	ATOM	127	CD	PRO	A	18	0	4.249	30.153	5.128	1.00	20.70
	ATOM	128	N	ASP	A	19	0	3.899	26.534	5.241	1.00	18.82
	ATOM	129	CA	ASP	A	19	0	3.323	25.227	5.475	1.00	16.87
25	ATOM	130	C	ASP	A	19	0	2.548	24.823	4.237	1.00	17.28
	ATOM	131	O	ASP	A	19	0	1.713	23.929	4.337	1.00	17.84
	ATOM	132	CB	ASP	A	19	0	2.419	25.207	6.701	1.00	16.54
	ATOM	133	CG	ASP	A	19	0	1.192	26.120	6.596	1.00	16.67
	ATOM	134	OD1	ASP	A	19	0	1.032	26.935	5.654	1.00	14.17
30	ATOM	135	OD2	ASP	A	19	0	0.360	26.045	7.529	1.00	14.56
	ATOM	136	N	GLY	A	20	0	2.782	25.469	3.100	1.00	17.87
	ATOM	137	CA	GLY	A	20	0	2.079	25.091	1.890	1.00	19.40
	ATOM	138	C	GLY	A	20	0	0.732	25.789	1.699	1.00	22.52
	ATOM	139	O	GLY	A	20	0	0.158	25.619	0.628	1.00	22.87
35	ATOM	140	N	PHE	A	21	0	0.240	26.587	2.631	1.00	21.35
	ATOM	141	CA	PHE	A	21	0	-0.913	27.443	2.534	1.00	20.39
	ATOM	142	C	PHE	A	21	0	-0.348	28.855	2.322	1.00	21.23
	ATOM	143	O	PHE	A	21	0	0.475	29.316	3.122	1.00	21.26

	ATOM	144	CB	PHE	A	21	0	-1.742	27.472	3.814	1.00	20.80
	ATOM	145	CG	PHE	A	21	0	-3.059	28.180	3.695	1.00	21.91
	ATOM	146	CD1	PHE	A	21	0	-3.171	29.527	3.963	1.00	22.49
	ATOM	147	CD2	PHE	A	21	0	-4.207	27.470	3.327	1.00	22.51
5	ATOM	148	CE1	PHE	A	21	0	-4.370	30.207	3.845	1.00	22.27
	ATOM	149	CE2	PHE	A	21	0	-5.419	28.128	3.203	1.00	22.79
	ATOM	150	CZ	PHE	A	21	0	-5.498	29.497	3.474	1.00	23.34
	ATOM	151	N	THR	A	22	0	-0.638	29.514	1.225	1.00	20.20
	ATOM	152	CA	THR	A	22	0	-0.143	30.850	0.977	1.00	21.36
10	ATOM	153	C	THR	A	22	0	-1.083	31.939	1.488	1.00	21.79
	ATOM	154	O	THR	A	22	0	-2.271	31.952	1.162	1.00	21.19
	ATOM	155	CB	THR	A	22	0	0.045	31.012	-0.553	1.00	21.46
	ATOM	156	OG1	THR	A	22	0	0.838	29.881	-0.934	1.00	20.09
	ATOM	157	CG2	THR	A	22	0	0.693	32.353	-0.891	1.00	20.94
15	ATOM	158	N	ARG	A	23	0	-0.562	32.871	2.257	1.00	20.80
	ATOM	159	CA	ARG	A	23	0	-1.230	34.008	2.844	1.00	20.78
	ATOM	160	C	ARG	A	23	0	-0.257	35.189	2.960	1.00	21.15
	ATOM	161	O	ARG	A	23	0	0.954	35.018	2.740	1.00	20.42
	ATOM	162	CB	ARG	A	23	0	-1.874	33.685	4.172	1.00	20.47
20	ATOM	163	CG	ARG	A	23	0	-0.964	33.152	5.295	1.00	21.52
	ATOM	164	CD	ARG	A	23	0	-0.552	34.357	6.113	1.00	22.75
	ATOM	165	NE	ARG	A	23	0	-0.905	34.419	7.477	1.00	21.60
	ATOM	166	CZ	ARG	A	23	0	-0.870	35.283	8.464	1.00	19.89
	ATOM	167	NH1	ARG	A	23	0	-0.526	36.565	8.453	1.00	20.19
25	ATOM	168	NH2	ARG	A	23	0	-1.249	34.744	9.610	1.00	18.64
	ATOM	169	N	ALA	A	24	0	-0.784	36.389	3.199	1.00	20.05
	ATOM	170	CA	ALA	A	24	0	0.140	37.541	3.243	1.00	22.03
	ATOM	171	C	ALA	A	24	0	0.786	37.561	4.635	1.00	21.09
	ATOM	172	O	ALA	A	24	0	0.200	37.124	5.637	1.00	21.16
30	ATOM	173	CB	ALA	A	24	0	-0.578	38.836	2.902	1.00	22.98
	ATOM	174	N	GLY	A	25	0	2.042	37.984	4.683	1.00	20.28
	ATOM	175	CA	GLY	A	25	0	2.786	37.993	5.950	1.00	20.29
	ATOM	176	C	GLY	A	25	0	3.649	39.254	5.979	1.00	21.38
	ATOM	177	O	GLY	A	25	0	3.465	40.229	5.238	1.00	21.06
35	ATOM	178	N	ILE	A	26	0	4.604	39.221	6.897	1.00	20.33
	ATOM	179	CA	ILE	A	26	0	5.475	40.365	7.145	1.00	20.64
	ATOM	180	C	ILE	A	26	0	6.903	39.886	6.932	1.00	20.00
	ATOM	181	O	ILE	A	26	0	7.247	38.851	7.485	1.00	21.34

	ATOM	182	CB	ILE	A	26	0	5.278	40.933	8.564	1.00	20.38
	ATOM	183	CG1	ILE	A	26	0	3.883	41.536	8.667	1.00	20.72
	ATOM	184	CG2	ILE	A	26	0	6.333	42.007	8.821	1.00	22.34
	ATOM	185	CD1	ILE	A	26	0	3.310	41.822	10.024	1.00	20.76
5	ATOM	186	N	LEU	A	27	0	7.644	40.551	6.079	1.00	19.10
	ATOM	187	CA	LEU	A	27	0	9.005	40.168	5.739	1.00	19.67
	ATOM	188	C	LEU	A	27	0	9.964	41.226	6.280	1.00	19.85
	ATOM	189	O	LEU	A	27	0	9.591	42.407	6.356	1.00	19.19
	ATOM	190	CB	LEU	A	27	0	9.138	40.172	4.219	1.00	20.26
10	ATOM	191	CG	LEU	A	27	0	9.046	38.883	3.415	1.00	22.65
	ATOM	192	CD1	LEU	A	27	0	8.127	37.835	3.989	1.00	21.10
	ATOM	193	CD2	LEU	A	27	0	8.738	39.198	1.963	1.00	22.01
	ATOM	194	N	VAL	A	28	0	11.162	40.804	6.630	1.00	18.03
	ATOM	195	CA	VAL	A	28	0	12.199	41.723	7.088	1.00	17.24
15	ATOM	196	C	VAL	A	28	0	13.289	41.573	6.040	1.00	18.99
	ATOM	197	O	VAL	A	28	0	13.791	40.453	5.863	1.00	20.36
	ATOM	198	CB	VAL	A	28	0	12.762	41.415	8.491	1.00	16.50
	ATOM	199	CG1	VAL	A	28	0	13.899	42.361	8.845	1.00	15.41
	ATOM	200	CG2	VAL	A	28	0	11.681	41.517	9.558	1.00	15.42
20	ATOM	201	N	ASN	A	29	0	13.575	42.601	5.256	1.00	20.78
	ATOM	202	CA	ASN	A	29	0	14.567	42.579	4.198	1.00	20.46
	ATOM	203	C	ASN	A	29	0	14.316	41.435	3.226	1.00	23.05
	ATOM	204	O	ASN	A	29	0	15.247	40.675	2.880	1.00	23.62
	ATOM	205	CB	ASN	A	29	0	15.982	42.446	4.764	1.00	21.06
25	ATOM	206	CG	ASN	A	29	0	16.475	43.654	5.522	1.00	22.44
	ATOM	207	OD1	ASN	A	29	0	15.870	44.722	5.434	1.00	23.47
	ATOM	208	ND2	ASN	A	29	0	17.560	43.507	6.288	1.00	22.23
	ATOM	209	N	GLY	A	30	0	13.053	41.215	2.878	1.00	23.18
	ATOM	210	CA	GLY	A	30	0	12.662	40.181	1.922	1.00	23.36
30	ATOM	211	C	GLY	A	30	0	12.723	38.757	2.436	1.00	23.85
	ATOM	212	O	GLY	A	30	0	12.707	37.814	1.633	1.00	25.17
	ATOM	213	N	VAL	A	31	0	12.832	38.585	3.755	1.00	21.85
	ATOM	214	CA	VAL	A	31	0	12.999	37.276	4.352	1.00	20.55
	ATOM	215	C	VAL	A	31	0	12.031	37.190	5.548	1.00	19.91
35	ATOM	216	O	VAL	A	31	0	11.796	38.172	6.269	1.00	17.50
	ATOM	217	CB	VAL	A	31	0	14.436	37.020	4.856	1.00	21.36
	ATOM	218	CG1	VAL	A	31	0	14.556	35.709	5.626	1.00	20.79
	ATOM	219	CG2	VAL	A	31	0	15.495	37.005	3.757	1.00	21.84

	ATOM	220	N	HIS A	32	0	11.489	35.984	5.698	1.00	17.05
	ATOM	221	CA	HIS A	32	0	10.592	35.729	6.797	1.00	18.61
	ATOM	222	C	HIS A	32	0	11.417	35.499	8.050	1.00	17.67
	ATOM	223	O	HIS A	32	0	11.873	34.385	8.216	1.00	18.72
5	ATOM	224	CB	HIS A	32	0	9.676	34.543	6.493	1.00	21.00
	ATOM	225	CG	HIS A	32	0	8.639	34.208	7.517	1.00	23.80
	ATOM	226	ND1	HIS A	32	0	7.744	33.174	7.332	1.00	25.14
	ATOM	227	CD2	HIS A	32	0	8.331	34.720	8.735	1.00	25.32
	ATOM	228	CE1	HIS A	32	0	6.942	33.061	8.385	1.00	25.36
10	ATOM	229	NE2	HIS A	32	0	7.271	33.986	9.260	1.00	26.23
	ATOM	230	N	GLY A	33	0	11.522	36.446	8.960	1.00	16.23
	ATOM	231	CA	GLY A	33	0	12.276	36.252	10.198	1.00	16.97
	ATOM	232	C	GLY A	33	0	13.740	35.869	10.083	1.00	15.54
	ATOM	233	O	GLY A	33	0	14.228	34.885	10.609	1.00	15.13
15	ATOM	234	N	PRO A	34	0	14.555	36.734	9.475	1.00	15.75
	ATOM	235	CA	PRO A	34	0	16.012	36.561	9.359	1.00	14.70
	ATOM	236	C	PRO A	34	0	16.734	36.660	10.701	1.00	14.02
	ATOM	237	O	PRO A	34	0	16.241	37.252	11.673	1.00	10.44
	ATOM	238	CB	PRO A	34	0	16.491	37.699	8.435	1.00	14.40
20	ATOM	239	CG	PRO A	34	0	15.441	38.742	8.783	1.00	15.11
	ATOM	240	CD	PRO A	34	0	14.113	38.005	8.905	1.00	13.69
	ATOM	241	N	LEU A	35	0	17.925	36.049	10.767	1.00	13.60
	ATOM	242	CA	LEU A	35	0	18.748	36.022	11.963	1.00	14.35
	ATOM	243	C	LEU A	35	0	19.462	37.359	12.161	1.00	16.25
25	ATOM	244	O	LEU A	35	0	20.015	37.902	11.210	1.00	14.10
	ATOM	245	CB	LEU A	35	0	19.834	34.916	11.862	1.00	15.33
	ATOM	246	CG	LEU A	35	0	20.958	34.943	12.911	1.00	17.74
	ATOM	247	CD1	LEU A	35	0	20.486	34.698	14.348	1.00	16.30
	ATOM	248	CD2	LEU A	35	0	22.052	33.934	12.575	1.00	16.60
30	ATOM	249	N	ILE A	36	0	19.471	37.855	13.384	1.00	16.71
	ATOM	250	CA	ILE A	36	0	20.265	39.027	13.738	1.00	16.66
	ATOM	251	C	ILE A	36	0	21.403	38.487	14.620	1.00	17.92
	ATOM	252	O	ILE A	36	0	21.183	37.732	15.573	1.00	17.20
	ATOM	253	CB	ILE A	36	0	19.560	40.129	14.533	1.00	16.60
35	ATOM	254	CG1	ILE A	36	0	18.389	40.771	13.771	1.00	16.09
	ATOM	255	CG2	ILE A	36	0	20.565	41.226	14.917	1.00	17.67
	ATOM	256	CD1	ILE A	36	0	17.590	41.754	14.629	1.00	15.88
	ATOM	257	N	ARG A	37	0	22.647	38.829	14.288	1.00	18.72

	ATOM	258	CA	ARG	A	37	0	23.754	38.315	15.091	1.00	19.94
	ATOM	259	C	ARG	A	37	0	24.839	39.369	15.280	1.00	20.08
	ATOM	260	O	ARG	A	37	0	24.979	40.249	14.450	1.00	20.52
	ATOM	261	CB	ARG	A	37	0	24.395	37.077	14.465	1.00	21.72
5	ATOM	262	CG	ARG	A	37	0	25.102	37.393	13.171	1.00	24.46
	ATOM	263	CD	ARG	A	37	0	26.113	36.339	12.762	1.00	26.90
	ATOM	264	NE	ARG	A	37	0	26.584	36.571	11.381	1.00	29.30
	ATOM	265	CZ	ARG	A	37	0	26.838	35.571	10.528	1.00	31.29
	ATOM	266	NH1	ARG	A	37	0	26.711	34.283	10.851	1.00	31.37
10	ATOM	267	NH2	ARG	A	37	0	27.252	35.827	9.291	1.00	31.66
	ATOM	268	N	GLY	A	38	0	25.587	39.223	16.361	1.00	20.22
	ATOM	269	CA	GLY	A	38	0	26.716	40.121	16.611	1.00	18.98
	ATOM	270	C	GLY	A	38	0	27.533	39.545	17.765	1.00	18.08
	ATOM	271	O	GLY	A	38	0	27.259	38.421	18.225	1.00	15.92
15	ATOM	272	N	GLY	A	39	0	28.436	40.412	18.238	1.00	17.65
	ATOM	273	CA	GLY	A	39	0	29.322	40.026	19.351	1.00	16.23
	ATOM	274	C	GLY	A	39	0	28.861	40.774	20.592	1.00	17.21
	ATOM	275	O	GLY	A	39	0	28.157	41.784	20.489	1.00	17.27
	ATOM	276	N	LYS	A	40	0	29.276	40.328	21.764	1.00	16.58
20	ATOM	277	CA	LYS	A	40	0	28.839	40.805	23.057	1.00	18.03
	ATOM	278	C	LYS	A	40	0	29.185	42.267	23.348	1.00	20.44
	ATOM	279	O	LYS	A	40	0	28.562	42.878	24.221	1.00	19.42
	ATOM	280	CB	LYS	A	40	0	29.394	39.933	24.185	1.00	16.74
	ATOM	281	CG	LYS	A	40	0	30.892	39.997	24.370	1.00	17.98
25	ATOM	282	CD	LYS	A	40	0	31.333	39.170	25.569	1.00	20.66
	ATOM	283	CE	LYS	A	40	0	32.809	38.768	25.493	1.00	21.70
	ATOM	284	NZ	LYS	A	40	0	33.227	38.111	26.757	1.00	23.11
	ATOM	285	N	ASN	A	41	0	30.181	42.780	22.645	1.00	21.43
	ATOM	286	CA	ASN	A	41	0	30.536	44.171	22.840	1.00	25.14
30	ATOM	287	C	ASN	A	41	0	30.092	44.976	21.644	1.00	24.05
	ATOM	288	O	ASN	A	41	0	30.409	46.161	21.655	1.00	25.66
	ATOM	289	CB	ASN	A	41	0	32.052	44.326	23.111	1.00	27.02
	ATOM	290	CG	ASN	A	41	0	32.434	43.606	24.404	1.00	29.76
	ATOM	291	OD1	ASN	A	41	0	33.398	42.832	24.431	1.00	31.54
35	ATOM	292	ND2	ASN	A	41	0	31.663	43.825	25.473	1.00	30.13
	ATOM	293	N	ASP	A	42	0	29.424	44.447	20.631	1.00	23.80
	ATOM	294	CA	ASP	A	42	0	29.073	45.325	19.506	1.00	24.12
	ATOM	295	C	ASP	A	42	0	28.169	46.484	19.891	1.00	24.24

	ATOM	296	O	ASP	A	42	0	27.420	46.428	20.872	1.00	22.42
	ATOM	297	CB	ASP	A	42	0	28.388	44.528	18.392	1.00	26.65
	ATOM	298	CG	ASP	A	42	0	29.404	43.599	17.773	1.00	28.94
	ATOM	299	OD1	ASP	A	42	0	30.603	43.754	18.056	1.00	31.45
5	ATOM	300	OD2	ASP	A	42	0	29.026	42.708	17.009	1.00	31.69
	ATOM	301	N	ASN	A	43	0	28.258	47.547	19.090	1.00	24.72
	ATOM	302	CA	ASN	A	43	0	27.316	48.660	19.255	1.00	26.50
	ATOM	303	C	ASN	A	43	0	26.293	48.430	18.128	1.00	26.23
	ATOM	304	O	ASN	A	43	0	26.723	48.420	16.979	1.00	25.02
10	ATOM	305	CB	ASN	A	43	0	27.934	50.047	19.128	1.00	28.45
	ATOM	306	CG	ASN	A	43	0	28.858	50.244	20.323	1.00	31.09
	ATOM	307	OD1	ASN	A	43	0	30.041	50.502	20.106	1.00	33.11
	ATOM	308	ND2	ASN	A	43	0	28.364	50.055	21.531	1.00	31.18
	ATOM	309	N	PHE	A	44	0	25.039	48.155	18.468	1.00	24.63
15	ATOM	310	CA	PHE	A	44	0	24.083	47.897	17.393	1.00	23.28
	ATOM	311	C	PHE	A	44	0	23.450	49.191	16.916	1.00	22.36
	ATOM	312	O	PHE	A	44	0	23.024	50.008	17.735	1.00	21.07
	ATOM	313	CB	PHE	A	44	0	22.959	46.965	17.853	1.00	22.04
	ATOM	314	CG	PHE	A	44	0	23.376	45.525	17.955	1.00	22.96
20	ATOM	315	CD1	PHE	A	44	0	22.779	44.562	17.153	1.00	23.91
	ATOM	316	CD2	PHE	A	44	0	24.330	45.120	18.869	1.00	22.03
	ATOM	317	CE1	PHE	A	44	0	23.131	43.230	17.253	1.00	24.42
	ATOM	318	CE2	PHE	A	44	0	24.689	43.797	18.974	1.00	23.25
	ATOM	319	CZ	PHE	A	44	0	24.095	42.837	18.168	1.00	24.02
25	ATOM	320	N	GLU	A	45	0	23.350	49.343	15.604	1.00	22.78
	ATOM	321	CA	GLU	A	45	0	22.611	50.482	15.054	1.00	24.47
	ATOM	322	C	GLU	A	45	0	21.619	49.884	14.055	1.00	23.79
	ATOM	323	O	GLU	A	45	0	22.017	49.587	12.924	1.00	24.40
	ATOM	324	CB	GLU	A	45	0	23.543	51.473	14.368	1.00	27.07
30	ATOM	325	CG	GLU	A	45	0	24.474	52.130	15.374	1.00	31.60
	ATOM	326	CD	GLU	A	45	0	25.380	53.179	14.772	1.00	33.90
	ATOM	327	OE1	GLU	A	45	0	25.354	53.438	13.559	1.00	35.62
	ATOM	328	OE2	GLU	A	45	0	26.155	53.748	15.565	1.00	36.42
	ATOM	329	N	LEU	A	46	0	20.369	49.684	14.465	1.00	22.18
35	ATOM	330	CA	LEU	A	46	0	19.419	49.044	13.556	1.00	21.22
	ATOM	331	C	LEU	A	46	0	18.348	50.001	13.077	1.00	21.27
	ATOM	332	O	LEU	A	46	0	17.464	50.429	13.812	1.00	21.60
	ATOM	333	CB	LEU	A	46	0	18.837	47.811	14.262	1.00	20.72

	ATOM	334	CG	LEU	A	46	0	19.827	46.658	14.403	1.00	21.28
	ATOM	335	CD1	LEU	A	46	0	19.334	45.621	15.397	1.00	20.83
	ATOM	336	CD2	LEU	A	46	0	20.148	46.034	13.052	1.00	18.33
	ATOM	337	N	ASN	A	47	0	18.438	50.403	11.823	1.00	21.09
5	ATOM	338	CA	ASN	A	47	0	17.498	51.344	11.252	1.00	22.37
	ATOM	339	C	ASN	A	47	0	16.273	50.558	10.803	1.00	22.18
	ATOM	340	O	ASN	A	47	0	16.390	49.810	9.847	1.00	23.41
	ATOM	341	CB	ASN	A	47	0	18.131	52.104	10.066	1.00	24.01
	ATOM	342	CG	ASN	A	47	0	17.226	53.243	9.615	1.00	25.54
10	ATOM	343	OD1	ASN	A	47	0	16.443	53.772	10.413	1.00	26.53
	ATOM	344	ND2	ASN	A	47	0	17.332	53.612	8.346	1.00	26.01
	ATOM	345	N	VAL	A	48	0	15.147	50.692	11.475	1.00	22.04
	ATOM	346	CA	VAL	A	48	0	13.918	49.995	11.140	1.00	21.99
	ATOM	347	C	VAL	A	48	0	13.026	50.879	10.269	1.00	21.82
15	ATOM	348	O	VAL	A	48	0	12.532	51.910	10.699	1.00	20.61
	ATOM	349	CB	VAL	A	48	0	13.176	49.579	12.430	1.00	22.64
	ATOM	350	CG1	VAL	A	48	0	11.819	48.931	12.148	1.00	21.99
	ATOM	351	CG2	VAL	A	48	0	14.098	48.631	13.216	1.00	21.68
	ATOM	352	N	VAL	A	49	0	12.931	50.512	9.009	1.00	21.79
20	ATOM	353	CA	VAL	A	49	0	12.164	51.167	7.966	1.00	21.34
	ATOM	354	C	VAL	A	49	0	10.816	50.460	7.795	1.00	21.12
	ATOM	355	O	VAL	A	49	0	10.703	49.308	7.365	1.00	19.76
	ATOM	356	CB	VAL	A	49	0	12.983	51.189	6.665	1.00	22.02
	ATOM	357	CG1	VAL	A	49	0	12.267	51.913	5.519	1.00	21.70
25	ATOM	358	CG2	VAL	A	49	0	14.312	51.933	6.906	1.00	21.47
	ATOM	359	N	ASN	A	50	0	9.767	51.112	8.257	1.00	20.26
	ATOM	360	CA	ASN	A	50	0	8.424	50.611	8.215	1.00	22.70
	ATOM	361	C	ASN	A	50	0	7.751	50.899	6.869	1.00	25.99
	ATOM	362	O	ASN	A	50	0	7.043	51.925	6.735	1.00	27.06
30	ATOM	363	CB	ASN	A	50	0	7.549	51.230	9.318	1.00	21.92
	ATOM	364	CG	ASN	A	50	0	6.198	50.569	9.471	1.00	22.44
	ATOM	365	OD1	ASN	A	50	0	5.818	49.801	8.572	1.00	24.19
	ATOM	366	ND2	ASN	A	50	0	5.435	50.833	10.526	1.00	20.19
	ATOM	367	N	ASP	A	51	0	7.915	49.959	5.926	1.00	26.42
35	ATOM	368	CA	ASP	A	51	0	7.208	50.071	4.641	1.00	26.35
	ATOM	369	C	ASP	A	51	0	5.951	49.200	4.600	1.00	24.86
	ATOM	370	O	ASP	A	51	0	5.542	48.810	3.511	1.00	25.19
	ATOM	371	CB	ASP	A	51	0	8.126	49.698	3.481	1.00	26.75

	ATOM	372	CG	ASP	A	51	0	9.152	50.761	3.158	1.00	29.77
	ATOM	373	OD1	ASP	A	51	0	8.944	51.904	3.617	1.00	31.03
	ATOM	374	OD2	ASP	A	51	0	10.166	50.509	2.465	1.00	30.42
	ATOM	375	N	LEU	A	52	0	5.332	48.801	5.700	1.00	25.05
5	ATOM	376	CA	LEU	A	52	0	4.172	47.911	5.640	1.00	25.44
	ATOM	377	C	LEU	A	52	0	2.934	48.624	5.094	1.00	26.65
	ATOM	378	O	LEU	A	52	0	2.553	49.696	5.586	1.00	24.56
	ATOM	379	CB	LEU	A	52	0	3.837	47.374	7.029	1.00	24.19
	ATOM	380	CG	LEU	A	52	0	4.896	46.503	7.699	1.00	24.60
10	ATOM	381	CD1	LEU	A	52	0	4.611	46.424	9.196	1.00	24.05
	ATOM	382	CD2	LEU	A	52	0	4.891	45.119	7.061	1.00	23.49
	ATOM	383	N	ASP	A	53	0	2.242	47.980	4.169	1.00	28.79
	ATOM	384	CA	ASP	A	53	0	1.049	48.602	3.581	1.00	29.91
	ATOM	385	C	ASP	A	53	0	-0.135	47.658	3.492	1.00	29.90
15	ATOM	386	O	ASP	A	53	0	-1.152	48.082	2.951	1.00	30.40
	ATOM	387	CB	ASP	A	53	0	1.367	49.190	2.197	1.00	29.26
	ATOM	388	CG	ASP	A	53	0	1.838	48.140	1.218	1.00	31.28
	ATOM	389	OD1	ASP	A	53	0	1.865	46.926	1.540	1.00	31.64
	ATOM	390	OD2	ASP	A	53	0	2.233	48.474	0.074	1.00	32.42
20	ATOM	391	N	ASN	A	54	0	-0.060	46.437	4.014	1.00	29.44
	ATOM	392	CA	ASN	A	54	0	-1.237	45.554	3.983	1.00	26.89
	ATOM	393	C	ASN	A	54	0	-2.089	45.832	5.192	1.00	27.37
	ATOM	394	O	ASN	A	54	0	-1.772	45.528	6.350	1.00	27.99
	ATOM	395	CB	ASN	A	54	0	-0.831	44.095	3.913	1.00	25.11
25	ATOM	396	CG	ASN	A	54	0	-1.978	43.141	3.690	1.00	24.20
	ATOM	397	OD1	ASN	A	54	0	-1.874	42.344	2.746	1.00	25.13
	ATOM	398	ND2	ASN	A	54	0	-3.030	43.182	4.481	1.00	23.26
	ATOM	399	N	PRO	A	55	0	-3.337	46.256	4.961	1.00	28.44
	ATOM	400	CA	PRO	A	55	0	-4.286	46.589	6.014	1.00	26.57
30	ATOM	401	C	PRO	A	55	0	-4.909	45.414	6.723	1.00	27.10
	ATOM	402	O	PRO	A	55	0	-5.671	45.624	7.687	1.00	26.05
	ATOM	403	CB	PRO	A	55	0	-5.368	47.465	5.334	1.00	28.18
	ATOM	404	CG	PRO	A	55	0	-5.249	47.049	3.899	1.00	27.50
	ATOM	405	CD	PRO	A	55	0	-3.844	46.564	3.625	1.00	27.56
35	ATOM	406	N	THR	A	56	0	-4.603	44.160	6.345	1.00	25.55
	ATOM	407	CA	THR	A	56	0	-5.214	43.024	7.065	1.00	25.52
	ATOM	408	C	THR	A	56	0	-4.446	42.647	8.326	1.00	24.87
	ATOM	409	O	THR	A	56	0	-4.766	41.764	9.115	1.00	23.97

	ATOM	410	CB	THR	A	56	0	-5.393	41.807	6.154	1.00	25.10
	ATOM	411	OG1	THR	A	56	0	-4.100	41.345	5.763	1.00	24.26
	ATOM	412	CG2	THR	A	56	0	-6.178	42.123	4.861	1.00	25.63
	ATOM	413	N	MET	A	57	0	-3.317	43.311	8.558	1.00	26.01
5	ATOM	414	CA	MET	A	57	0	-2.553	43.099	9.801	1.00	26.57
	ATOM	415	C	MET	A	57	0	-2.026	44.475	10.201	1.00	25.88
	ATOM	416	O	MET	A	57	0	-2.026	45.416	9.397	1.00	25.18
	ATOM	417	CB	MET	A	57	0	-1.561	41.939	9.698	1.00	25.42
	ATOM	418	CG	MET	A	57	0	-0.639	41.868	8.554	1.00	24.37
10	ATOM	419	SD	MET	A	57	0	-0.034	40.288	7.916	1.00	22.34
	ATOM	420	CE	MET	A	57	0	-0.275	40.640	6.167	1.00	19.23
	ATOM	421	N	LEU	A	58	0	-1.694	44.601	11.476	1.00	25.98
	ATOM	422	CA	LEU	A	58	0	-1.180	45.850	12.036	1.00	25.57
	ATOM	423	C	LEU	A	58	0	-0.053	46.425	11.195	1.00	24.52
15	ATOM	424	O	LEU	A	58	0	0.824	45.739	10.638	1.00	23.63
	ATOM	425	CB	LEU	A	58	0	-0.757	45.535	13.463	1.00	26.67
	ATOM	426	CG	LEU	A	58	0	-1.628	45.817	14.657	1.00	28.97
	ATOM	427	CD1	LEU	A	58	0	-3.107	45.995	14.312	1.00	30.99
	ATOM	428	CD2	LEU	A	58	0	-1.488	44.756	15.736	1.00	28.36
20	ATOM	429	N	ARG	A	59	0	-0.078	47.741	11.030	1.00	24.96
	ATOM	430	CA	ARG	A	59	0	0.918	48.434	10.231	1.00	26.92
	ATOM	431	C	ARG	A	59	0	1.932	49.229	11.014	1.00	26.31
	ATOM	432	O	ARG	A	59	0	3.120	49.198	10.699	1.00	28.82
	ATOM	433	CB	ARG	A	59	0	0.260	49.277	9.132	1.00	28.35
25	ATOM	434	CG	ARG	A	59	0	-0.252	48.385	7.986	1.00	29.50
	ATOM	435	CD	ARG	A	59	0	-0.986	49.274	6.996	1.00	30.33
	ATOM	436	NE	ARG	A	59	0	-2.333	49.604	7.459	1.00	32.26
	ATOM	437	CZ	ARG	A	59	0	-3.121	50.525	6.883	1.00	33.24
	ATOM	438	NH1	ARG	A	59	0	-2.679	51.233	5.845	1.00	32.27
30	ATOM	439	NH2	ARG	A	59	0	-4.340	50.712	7.389	1.00	32.65
	ATOM	440	N	PRO	A	60	0	1.542	49.961	12.020	1.00	26.30
	ATOM	441	CA	PRO	A	60	0	2.460	50.669	12.916	1.00	26.19
	ATOM	442	C	PRO	A	60	0	3.312	49.591	13.595	1.00	25.29
	ATOM	443	O	PRO	A	60	0	2.879	48.432	13.668	1.00	24.63
35	ATOM	444	CB	PRO	A	60	0	1.623	51.464	13.925	1.00	25.93
	ATOM	445	CG	PRO	A	60	0	0.235	51.357	13.325	1.00	26.19
	ATOM	446	CD	PRO	A	60	0	0.165	50.073	12.508	1.00	26.23
	ATOM	447	N	THR	A	61	0	4.544	49.932	13.976	1.00	24.60

	ATOM	448	CA	THR	A	61	O	5.365	48.871	14.587	1.00	23.49
	ATOM	449	C	THR	A	61	O	6.204	49.400	15.743	1.00	22.83
	ATOM	450	O	THR	A	61	O	6.390	50.601	15.921	1.00	20.77
	ATOM	451	CB	THR	A	61	O	6.245	48.170	13.535	1.00	22.69
5	ATOM	452	OG1	THR	A	61	O	6.668	46.918	14.096	1.00	23.55
	ATOM	453	CG2	THR	A	61	O	7.444	48.976	13.119	1.00	20.92
	ATOM	454	N	SER	A	62	O	6.702	48.449	16.507	1.00	22.38
	ATOM	455	CA	SER	A	62	O	7.599	48.672	17.633	1.00	22.47
	ATOM	456	C	SER	A	62	O	8.381	47.380	17.893	1.00	22.12
10	ATOM	457	O	SER	A	62	O	7.763	46.331	18.124	1.00	20.53
	ATOM	458	CB	SER	A	62	O	6.784	49.033	18.882	1.00	22.02
	ATOM	459	OG	SER	A	62	O	7.666	49.570	19.832	1.00	21.19
	ATOM	460	N	ILE	A	63	O	9.716	47.451	17.806	1.00	21.17
	ATOM	461	CA	ILE	A	63	O	10.513	46.240	17.960	1.00	18.32
15	ATOM	462	C	ILE	A	63	O	11.095	46.034	19.354	1.00	18.28
	ATOM	463	O	ILE	A	63	O	11.832	46.909	19.826	1.00	19.63
	ATOM	464	CB	ILE	A	63	O	11.642	46.234	16.924	1.00	16.68
	ATOM	465	CG1	ILE	A	63	O	11.166	46.509	15.508	1.00	18.51
	ATOM	466	CG2	ILE	A	63	O	12.319	44.848	16.906	1.00	16.78
20	ATOM	467	CD1	ILE	A	63	O	10.055	45.625	14.994	1.00	18.25
	ATOM	468	N	HIS	A	64	O	10.880	44.890	19.985	1.00	15.18
	ATOM	469	CA	HIS	A	64	O	11.478	44.539	21.261	1.00	15.51
	ATOM	470	C	HIS	A	64	O	12.648	43.559	21.029	1.00	16.73
	ATOM	471	O	HIS	A	64	O	12.491	42.591	20.279	1.00	16.85
25	ATOM	472	CB	HIS	A	64	O	10.512	43.912	22.239	1.00	14.37
	ATOM	473	CG	HIS	A	64	O	11.033	43.420	23.546	1.00	14.47
	ATOM	474	ND1	HIS	A	64	O	11.763	44.191	24.410	1.00	12.89
	ATOM	475	CD2	HIS	A	64	O	10.883	42.223	24.193	1.00	14.85
	ATOM	476	CE1	HIS	A	64	O	12.067	43.518	25.498	1.00	11.53
30	ATOM	477	NE2	HIS	A	64	O	11.547	42.325	25.423	1.00	13.63
	ATOM	478	N	TRP	A	65	O	13.761	43.781	21.723	1.00	14.37
	ATOM	479	CA	TRP	A	65	O	14.966	42.926	21.577	1.00	13.92
	ATOM	480	C	TRP	A	65	O	14.987	42.084	22.840	1.00	13.50
	ATOM	481	O	TRP	A	65	O	15.482	42.538	23.901	1.00	12.84
35	ATOM	482	CB	TRP	A	65	O	16.189	43.825	21.371	1.00	13.50
	ATOM	483	CG	TRP	A	65	O	15.890	45.020	20.492	1.00	13.19
	ATOM	484	CD1	TRP	A	65	O	15.453	46.247	20.913	1.00	12.42
	ATOM	485	CD2	TRP	A	65	O	15.908	45.087	19.068	1.00	13.61

	ATOM	486	NE1	TRP	A	65	0	15.234	47.067	19.862	1.00	11.49
	ATOM	487	CE2	TRP	A	65	0	15.511	46.390	18.710	1.00	13.77
	ATOM	488	CE3	TRP	A	65	0	16.251	44.174	18.061	1.00	14.35
	ATOM	489	CZ2	TRP	A	65	0	15.439	46.815	17.378	1.00	14.99
5	ATOM	490	CZ3	TRP	A	65	0	16.169	44.572	16.735	1.00	13.99
	ATOM	491	CH2	TRP	A	65	0	15.756	45.869	16.411	1.00	15.82
	ATOM	492	N	HIS	A	66	0	14.295	40.941	22.747	1.00	10.39
	ATOM	493	CA	HIS	A	66	0	13.939	40.200	23.966	1.00	12.00
	ATOM	494	C	HIS	A	66	0	15.158	39.653	24.698	1.00	11.34
10	ATOM	495	O	HIS	A	66	0	15.889	38.859	24.130	1.00	11.51
	ATOM	496	CB	HIS	A	66	0	12.923	39.069	23.629	1.00	10.76
	ATOM	497	CG	HIS	A	66	0	12.418	38.308	24.808	1.00	11.26
	ATOM	498	ND1	HIS	A	66	0	11.106	38.085	25.092	1.00	13.10
	ATOM	499	CD2	HIS	A	66	0	13.050	37.676	25.824	1.00	13.49
15	ATOM	500	CE1	HIS	A	66	0	10.919	37.407	26.191	1.00	12.50
	ATOM	501	NE2	HIS	A	66	0	12.116	37.146	26.683	1.00	13.71
	ATOM	502	N	GLY	A	67	0	15.345	39.971	25.948	1.00	12.84
	ATOM	503	CA	GLY	A	67	0	16.492	39.469	26.719	1.00	13.36
	ATOM	504	C	GLY	A	67	0	17.596	40.500	26.914	1.00	13.11
20	ATOM	505	O	GLY	A	67	0	18.435	40.289	27.788	1.00	13.36
	ATOM	506	N	LEU	A	68	0	17.641	41.558	26.131	1.00	12.89
	ATOM	507	CA	LEU	A	68	0	18.659	42.598	26.300	1.00	15.22
	ATOM	508	C	LEU	A	68	0	18.235	43.501	27.448	1.00	16.14
	ATOM	509	O	LEU	A	68	0	17.029	43.842	27.505	1.00	16.50
25	ATOM	510	CB	LEU	A	68	0	18.929	43.320	24.988	1.00	15.98
	ATOM	511	CG	LEU	A	68	0	20.002	42.638	24.114	1.00	19.57
	ATOM	512	CD1	LEU	A	68	0	19.719	41.185	23.809	1.00	20.39
	ATOM	513	CD2	LEU	A	68	0	20.188	43.316	22.758	1.00	19.59
	ATOM	514	N	PHE	A	69	0	19.125	43.848	28.386	1.00	13.24
30	ATOM	515	CA	PHE	A	69	0	18.700	44.657	29.526	1.00	13.85
	ATOM	516	C	PHE	A	69	0	18.499	46.128	29.205	1.00	14.34
	ATOM	517	O	PHE	A	69	0	17.806	46.879	29.895	1.00	15.02
	ATOM	518	CB	PHE	A	69	0	19.770	44.579	30.637	1.00	16.02
	ATOM	519	CG	PHE	A	69	0	20.112	43.187	31.072	1.00	16.45
35	ATOM	520	CD1	PHE	A	69	0	19.172	42.162	31.026	1.00	16.68
	ATOM	521	CD2	PHE	A	69	0	21.381	42.927	31.578	1.00	16.78
	ATOM	522	CE1	PHE	A	69	0	19.504	40.883	31.448	1.00	18.86
	ATOM	523	CE2	PHE	A	69	0	21.717	41.652	32.001	1.00	17.34

	ATOM	524	CZ	PHE	A	69	0	20.782	40.628	31.932	1.00	18.09
	ATOM	525	N	GLN	A	70	0	19.081	46.611	28.130	1.00	12.22
	ATOM	526	CA	GLN	A	70	0	18.919	47.990	27.708	1.00	15.20
	ATOM	527	C	GLN	A	70	0	19.242	49.004	28.799	1.00	16.76
5	ATOM	528	O	GLN	A	70	0	18.555	50.016	28.919	1.00	16.08
	ATOM	529	CB	GLN	A	70	0	17.488	48.115	27.232	1.00	15.52
	ATOM	530	CG	GLN	A	70	0	17.168	47.303	26.003	1.00	17.37
	ATOM	531	CD	GLN	A	70	0	17.781	47.744	24.709	1.00	17.70
	ATOM	532	OE1	GLN	A	70	0	17.557	47.090	23.676	1.00	21.63
10	ATOM	533	NE2	GLN	A	70	0	18.549	48.805	24.620	1.00	16.79
	ATOM	534	N	ARG	A	71	0	20.338	48.804	29.518	1.00	16.49
	ATOM	535	CA	ARG	A	71	0	20.765	49.712	30.588	1.00	18.41
	ATOM	536	C	ARG	A	71	0	21.239	51.011	29.970	1.00	16.23
	ATOM	537	O	ARG	A	71	0	22.059	50.998	29.027	1.00	14.48
15	ATOM	538	CB	ARG	A	71	0	21.827	48.942	31.382	1.00	22.65
	ATOM	539	CG	ARG	A	71	0	22.273	49.589	32.671	1.00	29.50
	ATOM	540	CD	ARG	A	71	0	23.286	48.756	33.457	1.00	32.92
	ATOM	541	NE	ARG	A	71	0	22.712	47.550	34.035	1.00	38.11
	ATOM	542	CZ	ARG	A	71	0	22.551	46.358	33.452	1.00	40.14
20	ATOM	543	NH1	ARG	A	71	0	22.939	46.138	32.190	1.00	41.23
	ATOM	544	NH2	ARG	A	71	0	22.022	45.333	34.130	1.00	40.89
	ATOM	545	N	GLY	A	72	0	20.613	52.145	30.311	1.00	14.82
	ATOM	546	CA	GLY	A	72	0	20.981	53.414	29.676	1.00	14.51
	ATOM	547	C	GLY	A	72	0	20.268	53.606	28.338	1.00	15.55
25	ATOM	548	O	GLY	A	72	0	20.401	54.706	27.777	1.00	16.32
	ATOM	549	N	THR	A	73	0	19.503	52.651	27.804	1.00	12.12
	ATOM	550	CA	THR	A	73	0	18.857	52.781	26.516	1.00	12.50
	ATOM	551	C	THR	A	73	0	17.418	52.252	26.621	1.00	13.98
	ATOM	552	O	THR	A	73	0	16.890	51.534	25.776	1.00	13.81
30	ATOM	553	CB	THR	A	73	0	19.577	52.086	25.346	1.00	12.21
	ATOM	554	OG1	THR	A	73	0	19.854	50.711	25.666	1.00	12.83
	ATOM	555	CG2	THR	A	73	0	20.944	52.711	25.000	1.00	9.81
	ATOM	556	N	ASN	A	74	0	16.744	52.617	27.708	1.00	12.97
	ATOM	557	CA	ASN	A	74	0	15.354	52.273	27.951	1.00	14.93
35	ATOM	558	C	ASN	A	74	0	14.469	52.718	26.784	1.00	15.92
	ATOM	559	O	ASN	A	74	0	13.501	52.030	26.455	1.00	16.56
	ATOM	560	CB	ASN	A	74	0	14.851	52.821	29.271	1.00	13.06
	ATOM	561	CG	ASN	A	74	0	13.385	52.519	29.556	1.00	15.47

	ATOM	562	OD1	ASN	A	74	0	12.557	53.250	29.021	1.00	13.99
	ATOM	563	ND2	ASN	A	74	0	13.063	51.500	30.367	1.00	13.91
	ATOM	564	N	TRP	A	75	0	14.806	53.765	26.041	1.00	16.16
	ATOM	565	CA	TRP	A	75	0	14.036	54.262	24.917	1.00	16.49
5	ATOM	566	C	TRP	A	75	0	14.050	53.345	23.701	1.00	17.29
	ATOM	567	O	TRP	A	75	0	13.235	53.529	22.776	1.00	16.34
	ATOM	568	CB	TRP	A	75	0	14.516	55.657	24.509	1.00	15.90
	ATOM	569	CG	TRP	A	75	0	15.990	55.705	24.207	1.00	16.04
	ATOM	570	CD1	TRP	A	75	0	17.011	55.972	25.072	1.00	14.90
10	ATOM	571	CD2	TRP	A	75	0	16.584	55.475	22.916	1.00	15.94
	ATOM	572	NE1	TRP	A	75	0	18.210	55.917	24.384	1.00	15.89
	ATOM	573	CE2	TRP	A	75	0	17.977	55.624	23.076	1.00	15.80
	ATOM	574	CE3	TRP	A	75	0	16.060	55.171	21.656	1.00	14.88
	ATOM	575	CZ2	TRP	A	75	0	18.867	55.459	22.016	1.00	17.60
15	ATOM	576	CZ3	TRP	A	75	0	16.928	55.025	20.603	1.00	16.64
	ATOM	577	CH2	TRP	A	75	0	18.321	55.153	20.785	1.00	18.16
	ATOM	578	N	ALA	A	76	0	14.962	52.372	23.675	1.00	15.12
	ATOM	579	CA	ALA	A	76	0	15.075	51.430	22.578	1.00	14.61
	ATOM	580	C	ALA	A	76	0	14.569	50.047	22.971	1.00	13.98
20	ATOM	581	O	ALA	A	76	0	14.617	49.132	22.159	1.00	14.20
	ATOM	582	CB	ALA	A	76	0	16.554	51.354	22.157	1.00	13.68
	ATOM	583	N	ASP	A	77	0	13.941	49.885	24.121	1.00	14.47
	ATOM	584	CA	ASP	A	77	0	13.409	48.605	24.586	1.00	14.23
	ATOM	585	C	ASP	A	77	0	12.198	48.167	23.762	1.00	15.04
25	ATOM	586	O	ASP	A	77	0	11.982	46.946	23.638	1.00	13.78
	ATOM	587	CB	ASP	A	77	0	13.112	48.567	26.072	1.00	13.41
	ATOM	588	CG	ASP	A	77	0	12.945	47.155	26.612	1.00	14.93
	ATOM	589	OD1	ASP	A	77	0	11.943	46.986	27.345	1.00	15.07
	ATOM	590	OD2	ASP	A	77	0	13.744	46.217	26.334	1.00	13.73
30	ATOM	591	N	GLY	A	78	0	11.458	49.095	23.160	1.00	13.63
	ATOM	592	CA	GLY	A	78	0	10.442	48.686	22.210	1.00	14.96
	ATOM	593	C	GLY	A	78	0	9.040	48.309	22.631	1.00	16.75
	ATOM	594	O	GLY	A	78	0	8.276	47.865	21.755	1.00	16.49
	ATOM	595	N	ALA	A	79	0	8.631	48.436	23.886	1.00	15.34
35	ATOM	596	CA	ALA	A	79	0	7.252	48.176	24.270	1.00	14.70
	ATOM	597	C	ALA	A	79	0	6.490	49.495	24.084	1.00	17.51
	ATOM	598	O	ALA	A	79	0	6.690	50.486	24.807	1.00	17.05
	ATOM	599	CB	ALA	A	79	0	7.145	47.701	25.708	1.00	14.78

	ATOM	600	N	ASP	A	80	0	5.641	49.536	23.053	1.00	18.56
	ATOM	601	CA	ASP	A	80	0	4.859	50.741	22.798	1.00	19.52
	ATOM	602	C	ASP	A	80	0	3.959	50.963	24.010	1.00	17.61
	ATOM	603	O	ASP	A	80	0	3.530	49.999	24.664	1.00	16.72
5	ATOM	604	CB	ASP	A	80	0	4.044	50.714	21.510	1.00	24.02
	ATOM	605	CG	ASP	A	80	0	3.003	49.607	21.549	1.00	28.13
	ATOM	606	OD1	ASP	A	80	0	3.410	48.417	21.541	1.00	30.66
	ATOM	607	OD2	ASP	A	80	0	1.803	49.959	21.603	1.00	30.61
	ATOM	608	N	GLY	A	81	0	3.776	52.242	24.337	1.00	15.85
10	ATOM	609	CA	GLY	A	81	0	2.991	52.566	25.532	1.00	16.27
	ATOM	610	C	GLY	A	81	0	3.846	52.615	26.784	1.00	18.72
	ATOM	611	O	GLY	A	81	0	3.405	52.983	27.890	1.00	20.61
	ATOM	612	N	VAL	A	82	0	5.108	52.173	26.725	1.00	19.11
	ATOM	613	CA	VAL	A	82	0	5.978	52.119	27.890	1.00	19.14
15	ATOM	614	C	VAL	A	82	0	7.288	52.851	27.590	1.00	18.41
	ATOM	615	O	VAL	A	82	0	7.594	53.839	28.242	1.00	16.79
	ATOM	616	CB	VAL	A	82	0	6.266	50.697	28.390	1.00	19.82
	ATOM	617	CG1	VAL	A	82	0	7.059	50.741	29.710	1.00	21.37
	ATOM	618	CG2	VAL	A	82	0	4.995	49.894	28.640	1.00	19.27
20	ATOM	619	N	ASN	A	83	0	7.982	52.408	26.551	1.00	17.90
	ATOM	620	CA	ASN	A	83	0	9.271	52.926	26.147	1.00	16.94
	ATOM	621	C	ASN	A	83	0	9.226	53.778	24.886	1.00	18.32
	ATOM	622	O	ASN	A	83	0	10.175	54.551	24.634	1.00	20.58
	ATOM	623	CB	ASN	A	83	0	10.249	51.747	25.937	1.00	15.23
25	ATOM	624	CG	ASN	A	83	0	10.112	50.745	27.063	1.00	16.00
	ATOM	625	OD1	ASN	A	83	0	9.493	49.676	26.879	1.00	14.98
	ATOM	626	ND2	ASN	A	83	0	10.583	51.131	28.249	1.00	13.17
	ATOM	627	N	GLN	A	84	0	8.183	53.668	24.066	1.00	16.40
	ATOM	628	CA	GLN	A	84	0	8.080	54.464	22.867	1.00	16.34
30	ATOM	629	C	GLN	A	84	0	6.658	54.465	22.309	1.00	17.95
	ATOM	630	O	GLN	A	84	0	5.816	53.679	22.728	1.00	17.69
	ATOM	631	CB	GLN	A	84	0	8.995	53.953	21.754	1.00	17.98
	ATOM	632	CG	GLN	A	84	0	8.456	52.654	21.127	1.00	16.63
	ATOM	633	CD	GLN	A	84	0	9.272	52.225	19.938	1.00	18.17
35	ATOM	634	OE1	GLN	A	84	0	8.994	52.601	18.792	1.00	20.91
	ATOM	635	NE2	GLN	A	84	0	10.279	51.385	20.096	1.00	18.70
	ATOM	636	N	CYS	A	85	0	6.419	55.350	21.365	1.00	18.60
	ATOM	637	CA	CYS	A	85	0	5.140	55.344	20.622	1.00	20.25

	ATOM	638	C	CYS A	85	0	5.512	54.555	19.375	1.00	19.55
	ATOM	639	O	CYS A	85	0	6.690	54.546	18.995	1.00	18.92
	ATOM	640	CB	CYS A	85	0	4.772	56.786	20.228	1.00	22.20
	ATOM	641	SG	CYS A	85	0	3.899	57.783	21.481	1.00	24.65
5	ATOM	642	N	PRO A	86	0	4.589	53.951	18.674	1.00	21.19
	ATOM	643	CA	PRO A	86	0	4.869	53.152	17.498	1.00	20.78
	ATOM	644	C	PRO A	86	0	5.560	53.930	16.394	1.00	21.46
	ATOM	645	O	PRO A	86	0	5.453	55.137	16.298	1.00	23.08
	ATOM	646	CB	PRO A	86	0	3.530	52.555	17.028	1.00	19.94
10	ATOM	647	CG	PRO A	86	0	2.667	52.720	18.252	1.00	19.59
	ATOM	648	CD	PRO A	86	0	3.174	53.872	19.062	1.00	20.46
	ATOM	649	N	ILE A	87	0	6.318	53.259	15.550	1.00	20.95
	ATOM	650	CA	ILE A	87	0	6.907	53.773	14.337	1.00	22.43
	ATOM	651	C	ILE A	87	0	5.768	53.641	13.292	1.00	22.80
15	ATOM	652	O	ILE A	87	0	5.148	52.562	13.228	1.00	21.61
	ATOM	653	CB	ILE A	87	0	8.105	52.954	13.844	1.00	21.99
	ATOM	654	CG1	ILE A	87	0	9.130	52.696	14.944	1.00	24.18
	ATOM	655	CG2	ILE A	87	0	8.773	53.656	12.674	1.00	22.91
	ATOM	656	CD1	ILE A	87	0	10.256	51.776	14.514	1.00	23.87
20	ATOM	657	N	SER A	88	0	5.464	54.702	12.570	1.00	22.64
	ATOM	658	CA	SER A	88	0	4.338	54.709	11.647	1.00	22.85
	ATOM	659	C	SER A	88	0	4.751	54.268	10.249	1.00	23.35
	ATOM	660	O	SER A	88	0	5.870	54.489	9.764	1.00	23.30
	ATOM	661	CB	SER A	88	0	3.767	56.137	11.518	1.00	24.00
25	ATOM	662	OG	SER A	88	0	3.379	56.770	12.720	1.00	23.93
	ATOM	663	N	PRO A	89	0	3.778	53.752	9.514	1.00	23.60
	ATOM	664	CA	PRO A	89	0	3.955	53.382	8.116	1.00	25.19
	ATOM	665	C	PRO A	89	0	4.579	54.556	7.361	1.00	26.58
	ATOM	666	O	PRO A	89	0	4.177	55.699	7.585	1.00	26.66
30	ATOM	667	CB	PRO A	89	0	2.566	53.065	7.555	1.00	23.59
	ATOM	668	CG	PRO A	89	0	1.740	52.856	8.798	1.00	22.37
	ATOM	669	CD	PRO A	89	0	2.415	53.513	9.970	1.00	23.25
	ATOM	670	N	GLY A	90	0	5.588	54.311	6.550	1.00	27.73
	ATOM	671	CA	GLY A	90	0	6.223	55.338	5.748	1.00	30.55
35	ATOM	672	C	GLY A	90	0	7.384	56.032	6.438	1.00	32.38
	ATOM	673	O	GLY A	90	0	8.050	56.894	5.879	1.00	32.53
	ATOM	674	N	HIS A	91	0	7.639	55.693	7.702	1.00	32.77
	ATOM	675	CA	HIS A	91	0	8.691	56.283	8.494	1.00	32.55

	ATOM	676	C	HIS	A	91	0	9.649	55.179	8.982	1.00	32.36
	ATOM	677	O	HIS	A	91	0	9.381	53.972	8.961	1.00	31.30
	ATOM	678	CB	HIS	A	91	0	8.118	57.016	9.722	1.00	33.75
	ATOM	679	CG	HIS	A	91	0	7.147	58.073	9.295	1.00	34.64
5	ATOM	680	ND1	HIS	A	91	0	7.519	59.381	9.072	1.00	34.41
	ATOM	681	CD2	HIS	A	91	0	5.822	57.977	9.002	1.00	34.89
	ATOM	682	CE1	HIS	A	91	0	6.450	60.050	8.679	1.00	34.87
	ATOM	683	NE2	HIS	A	91	0	5.410	59.233	8.628	1.00	35.14
	ATOM	684	N	ALA	A	92	0	10.786	55.668	9.437	1.00	29.57
10	ATOM	685	CA	ALA	A	92	0	11.895	54.898	9.937	1.00	27.71
	ATOM	686	C	ALA	A	92	0	12.316	55.347	11.337	1.00	27.41
	ATOM	687	O	ALA	A	92	0	12.076	56.484	11.741	1.00	26.12
	ATOM	688	CB	ALA	A	92	0	13.051	55.057	8.967	1.00	25.23
	ATOM	689	N	PHE	A	93	0	12.931	54.418	12.081	1.00	26.87
15	ATOM	690	CA	PHE	A	93	0	13.441	54.760	13.405	1.00	25.87
	ATOM	691	C	PHE	A	93	0	14.746	54.008	13.632	1.00	25.21
	ATOM	692	O	PHE	A	93	0	14.797	52.810	13.347	1.00	25.80
	ATOM	693	CB	PHE	A	93	0	12.457	54.456	14.526	1.00	25.30
	ATOM	694	CG	PHE	A	93	0	12.964	54.955	15.847	1.00	25.41
20	ATOM	695	CD1	PHE	A	93	0	13.154	56.309	16.061	1.00	25.36
	ATOM	696	CD2	PHE	A	93	0	13.276	54.057	16.853	1.00	25.31
	ATOM	697	CE1	PHE	A	93	0	13.637	56.753	17.285	1.00	26.54
	ATOM	698	CE2	PHE	A	93	0	13.754	54.503	18.078	1.00	25.39
	ATOM	699	CZ	PHE	A	93	0	13.935	55.857	18.302	1.00	25.01
25	ATOM	700	N	LEU	A	94	0	15.756	54.699	14.136	1.00	23.39
	ATOM	701	CA	LEU	A	94	0	17.046	54.058	14.361	1.00	23.35
	ATOM	702	C	LEU	A	94	0	17.191	53.611	15.804	1.00	23.22
	ATOM	703	O	LEU	A	94	0	17.261	54.431	16.714	1.00	23.47
	ATOM	704	CB	LEU	A	94	0	18.186	54.994	13.943	1.00	24.96
30	ATOM	705	CG	LEU	A	94	0	19.630	54.555	14.170	1.00	26.28
	ATOM	706	CD1	LEU	A	94	0	19.979	53.313	13.352	1.00	25.99
	ATOM	707	CD2	LEU	A	94	0	20.627	55.678	13.887	1.00	26.06
	ATOM	708	N	TYR	A	95	0	17.261	52.293	16.023	1.00	21.81
	ATOM	709	CA	TYR	A	95	0	17.481	51.780	17.379	1.00	19.72
35	ATOM	710	C	TYR	A	95	0	18.991	51.663	17.585	1.00	20.90
	ATOM	711	O	TYR	A	95	0	19.690	51.248	16.656	1.00	20.74
	ATOM	712	CB	TYR	A	95	0	16.831	50.448	17.609	1.00	17.86
	ATOM	713	CG	TYR	A	95	0	15.329	50.411	17.691	1.00	16.35

	ATOM	714	CD1	TYR	A	95	0	14.541	50.288	16.535	1.00	16.89
	ATOM	715	CD2	TYR	A	95	0	14.701	50.442	18.911	1.00	15.71
	ATOM	716	CE1	TYR	A	95	0	13.157	50.205	16.621	1.00	17.21
	ATOM	717	CE2	TYR	A	95	0	13.325	50.362	19.033	1.00	16.25
5	ATOM	718	CZ	TYR	A	95	0	12.568	50.266	17.874	1.00	17.97
	ATOM	719	OH	TYR	A	95	0	11.205	50.189	18.001	1.00	18.61
	ATOM	720	N	LYS	A	96	0	19.475	52.105	18.752	1.00	20.56
	ATOM	721	CA	LYS	A	96	0	20.917	52.058	18.975	1.00	21.77
	ATOM	722	C	LYS	A	96	0	21.139	51.519	20.386	1.00	20.91
10	ATOM	723	O	LYS	A	96	0	20.558	52.122	21.286	1.00	21.98
	ATOM	724	CB	LYS	A	96	0	21.565	53.427	18.960	1.00	22.89
	ATOM	725	CG	LYS	A	96	0	21.857	54.046	17.609	1.00	26.39
	ATOM	726	CD	LYS	A	96	0	22.749	55.251	17.923	1.00	30.80
	ATOM	727	CE	LYS	A	96	0	22.732	56.348	16.884	1.00	32.90
15	ATOM	728	NZ	LYS	A	96	0	23.767	57.378	17.277	1.00	36.06
	ATOM	729	N	PHE	A	97	0	21.871	50.437	20.520	1.00	18.14
	ATOM	730	CA	PHE	A	97	0	22.062	49.863	21.854	1.00	18.19
	ATOM	731	C	PHE	A	97	0	23.276	48.928	21.805	1.00	16.76
	ATOM	732	O	PHE	A	97	0	23.870	48.700	20.747	1.00	14.19
20	ATOM	733	CB	PHE	A	97	0	20.816	49.067	22.307	1.00	17.34
	ATOM	734	CG	PHE	A	97	0	20.379	48.026	21.304	1.00	17.56
	ATOM	735	CD1	PHE	A	97	0	20.873	46.732	21.348	1.00	16.27
	ATOM	736	CD2	PHE	A	97	0	19.451	48.343	20.326	1.00	18.65
	ATOM	737	CE1	PHE	A	97	0	20.476	45.801	20.398	1.00	17.76
25	ATOM	738	CE2	PHE	A	97	0	19.026	47.408	19.386	1.00	18.64
	ATOM	739	CZ	PHE	A	97	0	19.546	46.120	19.416	1.00	17.55
	ATOM	740	N	THR	A	98	0	23.552	48.348	22.971	1.00	17.45
	ATOM	741	CA	THR	A	98	0	24.644	47.359	22.992	1.00	17.00
	ATOM	742	C	THR	A	98	0	24.304	46.333	24.042	1.00	16.63
30	ATOM	743	O	THR	A	98	0	23.725	46.631	25.090	1.00	15.86
	ATOM	744	CB	THR	A	98	0	26.028	47.990	23.256	1.00	17.53
	ATOM	745	OG1	THR	A	98	0	27.017	46.924	23.372	1.00	19.01
	ATOM	746	CG2	THR	A	98	0	26.088	48.807	24.525	1.00	14.85
	ATOM	747	N	PRO	A	99	0	24.740	45.097	23.831	1.00	15.98
35	ATOM	748	CA	PRO	A	99	0	24.601	44.019	24.787	1.00	15.11
	ATOM	749	C	PRO	A	99	0	25.445	44.270	26.020	1.00	15.99
	ATOM	750	O	PRO	A	99	0	25.260	43.633	27.064	1.00	15.94
	ATOM	751	CB	PRO	A	99	0	25.025	42.717	24.098	1.00	15.83

	ATOM	752	CG	PRO	A	99	0	25.042	43.140	22.644	1.00	17.12
	ATOM	753	CD	PRO	A	99	0	25.362	44.627	22.601	1.00	15.68
	ATOM	754	N	ALA	A	100	0	26.452	45.149	25.932	1.00	17.29
	ATOM	755	CA	ALA	A	100	0	27.316	45.501	27.050	1.00	16.88
5	ATOM	756	C	ALA	A	100	0	27.919	44.293	27.754	1.00	16.16
	ATOM	757	O	ALA	A	100	0	27.779	44.187	28.977	1.00	18.13
	ATOM	758	CB	ALA	A	100	0	26.498	46.292	28.084	1.00	14.96
	ATOM	759	N	GLY	A	101	0	28.474	43.360	27.033	1.00	16.41
	ATOM	760	CA	GLY	A	101	0	29.063	42.172	27.599	1.00	17.49
10	ATOM	761	C	GLY	A	101	0	28.130	40.994	27.769	1.00	16.15
	ATOM	762	O	GLY	A	101	0	28.593	39.930	28.137	1.00	16.57
	ATOM	763	N	HIS	A	102	0	26.838	41.120	27.521	1.00	17.58
	ATOM	764	CA	HIS	A	102	0	25.858	40.058	27.804	1.00	15.77
	ATOM	765	C	HIS	A	102	0	25.707	39.165	26.600	1.00	15.28
15	ATOM	766	O	HIS	A	102	0	25.087	39.641	25.662	1.00	17.64
	ATOM	767	CB	HIS	A	102	0	24.498	40.666	28.186	1.00	17.95
	ATOM	768	CG	HIS	A	102	0	23.432	39.661	28.493	1.00	20.00
	ATOM	769	ND1	HIS	A	102	0	22.099	40.005	28.547	1.00	20.59
	ATOM	770	CD2	HIS	A	102	0	23.475	38.323	28.772	1.00	20.09
20	ATOM	771	CE1	HIS	A	102	0	21.398	38.937	28.866	1.00	20.77
	ATOM	772	NE2	HIS	A	102	0	22.201	37.896	29.016	1.00	20.56
	ATOM	773	N	ALA	A	103	0	26.277	37.958	26.584	1.00	13.32
	ATOM	774	CA	ALA	A	103	0	26.141	37.127	25.415	1.00	13.99
	ATOM	775	C	ALA	A	103	0	24.974	36.156	25.649	1.00	13.43
25	ATOM	776	O	ALA	A	103	0	24.571	35.905	26.784	1.00	11.81
	ATOM	777	CB	ALA	A	103	0	27.418	36.329	25.151	1.00	16.36
	ATOM	778	N	GLY	A	104	0	24.459	35.610	24.554	1.00	12.38
	ATOM	779	CA	GLY	A	104	0	23.381	34.632	24.778	1.00	12.85
	ATOM	780	C	GLY	A	104	0	22.480	34.451	23.581	1.00	11.06
30	ATOM	781	O	GLY	A	104	0	22.674	35.057	22.515	1.00	10.91
	ATOM	782	N	THR	A	105	0	21.442	33.650	23.794	1.00	10.14
	ATOM	783	CA	THR	A	105	0	20.490	33.394	22.704	1.00	10.04
	ATOM	784	C	THR	A	105	0	19.238	34.236	22.989	1.00	9.52
	ATOM	785	O	THR	A	105	0	18.738	34.194	24.125	1.00	7.52
35	ATOM	786	CB	THR	A	105	0	20.114	31.913	22.665	1.00	12.67
	ATOM	787	OG1	THR	A	105	0	21.273	31.075	22.593	1.00	13.47
	ATOM	788	CG2	THR	A	105	0	19.187	31.684	21.468	1.00	12.75
	ATOM	789	N	PHE	A	106	0	18.842	35.065	22.044	1.00	7.76

	ATOM	790	CA	PHE	A	106	0	17.731	35.992	22.243	1.00	10.15
	ATOM	791	C	PHE	A	106	0	16.756	35.910	21.068	1.00	8.42
	ATOM	792	O	PHE	A	106	0	16.941	35.083	20.166	1.00	8.33
	ATOM	793	CB	PHE	A	106	0	18.283	37.460	22.369	1.00	10.19
5	ATOM	794	CG	PHE	A	106	0	19.291	37.577	23.506	1.00	12.95
	ATOM	795	CD1	PHE	A	106	0	18.905	37.443	24.815	1.00	11.44
	ATOM	796	CD2	PHE	A	106	0	20.654	37.775	23.230	1.00	12.37
	ATOM	797	CE1	PHE	A	106	0	19.855	37.531	25.822	1.00	14.20
	ATOM	798	CE2	PHE	A	106	0	21.574	37.857	24.273	1.00	11.56
10	ATOM	799	CZ	PHE	A	106	0	21.202	37.733	25.599	1.00	9.45
	ATOM	800	N	TRP	A	107	0	15.869	36.887	20.917	1.00	6.61
	ATOM	801	CA	TRP	A	107	0	15.062	36.977	19.713	1.00	10.20
	ATOM	802	C	TRP	A	107	0	14.511	38.398	19.625	1.00	10.63
	ATOM	803	O	TRP	A	107	0	14.463	39.036	20.657	1.00	13.71
15	ATOM	804	CB	TRP	A	107	0	13.928	35.966	19.636	1.00	7.49
	ATOM	805	CG	TRP	A	107	0	12.945	35.916	20.755	1.00	9.41
	ATOM	806	CD1	TRP	A	107	0	13.136	35.804	22.106	1.00	10.53
	ATOM	807	CD2	TRP	A	107	0	11.509	36.004	20.581	1.00	9.17
	ATOM	808	NE1	TRP	A	107	0	11.929	35.784	22.768	1.00	10.63
20	ATOM	809	CE2	TRP	A	107	0	10.924	35.926	21.842	1.00	9.90
	ATOM	810	CE3	TRP	A	107	0	10.698	36.144	19.444	1.00	8.77
	ATOM	811	CZ2	TRP	A	107	0	9.538	35.947	22.025	1.00	10.01
	ATOM	812	CZ3	TRP	A	107	0	9.336	36.167	19.613	1.00	8.60
	ATOM	813	CH2	TRP	A	107	0	8.774	36.061	20.890	1.00	10.09
25	ATOM	814	N	TYR	A	108	0	14.117	38.847	18.464	1.00	10.72
	ATOM	815	CA	TYR	A	108	0	13.498	40.148	18.302	1.00	12.19
	ATOM	816	C	TYR	A	108	0	12.030	39.869	17.875	1.00	13.62
	ATOM	817	O	TYR	A	108	0	11.752	38.837	17.245	1.00	13.85
	ATOM	818	CB	TYR	A	108	0	14.182	40.994	17.259	1.00	11.05
30	ATOM	819	CG	TYR	A	108	0	14.176	40.413	15.857	1.00	13.89
	ATOM	820	CD1	TYR	A	108	0	15.087	39.464	15.423	1.00	12.99
	ATOM	821	CD2	TYR	A	108	0	13.257	40.897	14.920	1.00	14.94
	ATOM	822	CE1	TYR	A	108	0	15.064	38.979	14.130	1.00	13.64
	ATOM	823	CE2	TYR	A	108	0	13.216	40.409	13.624	1.00	15.34
35	ATOM	824	CZ	TYR	A	108	0	14.123	39.443	13.236	1.00	14.99
	ATOM	825	OH	TYR	A	108	0	14.063	38.960	11.946	1.00	16.68
	ATOM	826	N	HIS	A	109	0	11.123	40.752	18.254	1.00	12.81
	ATOM	827	CA	HIS	A	109	0	9.735	40.630	17.826	1.00	14.92

	ATOM	828	C	HIS A 109	0	9.057	41.988	17.991	1.00	15.96
	ATOM	829	O	HIS A 109	0	9.392	42.800	18.875	1.00	15.67
	ATOM	830	CB	HIS A 109	0	8.903	39.566	18.550	1.00	12.30
	ATOM	831	CG	HIS A 109	0	8.804	39.727	20.036	1.00	12.30
5	ATOM	832	ND1	HIS A 109	0	7.788	40.429	20.666	1.00	9.89
	ATOM	833	CD2	HIS A 109	0	9.614	39.264	21.034	1.00	10.76
	ATOM	834	CE1	HIS A 109	0	7.982	40.379	21.971	1.00	8.49
	ATOM	835	NE2	HIS A 109	0	9.086	39.679	22.224	1.00	7.92
	ATOM	836	N	SER A 110	0	8.070	42.203	17.122	1.00	16.26
10	ATOM	837	CA	SER A 110	0	7.244	43.404	17.300	1.00	14.55
	ATOM	838	C	SER A 110	0	6.548	43.283	18.646	1.00	13.56
	ATOM	839	O	SER A 110	0	6.219	42.191	19.140	1.00	13.54
	ATOM	840	CB	SER A 110	0	6.219	43.543	16.159	1.00	16.69
	ATOM	841	OG	SER A 110	0	5.212	44.481	16.508	1.00	15.32
15	ATOM	842	N	HIS A 111	0	6.396	44.395	19.359	1.00	14.60
	ATOM	843	CA	HIS A 111	0	5.724	44.397	20.645	1.00	16.23
	ATOM	844	C	HIS A 111	0	4.349	45.070	20.478	1.00	18.61
	ATOM	845	O	HIS A 111	0	3.713	45.391	21.473	1.00	21.72
	ATOM	846	CB	HIS A 111	0	6.478	45.166	21.721	1.00	14.37
20	ATOM	847	CG	HIS A 111	0	6.392	44.519	23.077	1.00	15.33
	ATOM	848	ND1	HIS A 111	0	5.341	44.660	23.947	1.00	14.55
	ATOM	849	CD2	HIS A 111	0	7.265	43.676	23.680	1.00	14.72
	ATOM	850	CE1	HIS A 111	0	5.589	43.936	25.040	1.00	16.29
	ATOM	851	NE2	HIS A 111	0	6.773	43.326	24.920	1.00	15.35
25	ATOM	852	N	PHE A 112	0	3.950	45.382	19.258	1.00	18.67
	ATOM	853	CA	PHE A 112	0	2.725	46.139	19.037	1.00	19.61
	ATOM	854	C	PHE A 112	0	1.540	45.219	18.777	1.00	19.06
	ATOM	855	O	PHE A 112	0	1.521	44.630	17.707	1.00	17.50
	ATOM	856	CB	PHE A 112	0	2.971	47.113	17.875	1.00	21.16
30	ATOM	857	CG	PHE A 112	0	1.798	48.019	17.611	1.00	23.12
	ATOM	858	CD1	PHE A 112	0	1.456	49.007	18.509	1.00	24.59
	ATOM	859	CD2	PHE A 112	0	1.034	47.886	16.466	1.00	24.82
	ATOM	860	CE1	PHE A 112	0	0.387	49.852	18.312	1.00	24.29
	ATOM	861	CE2	PHE A 112	0	-0.063	48.714	16.243	1.00	25.87
35	ATOM	862	CZ	PHE A 112	0	-0.378	49.698	17.161	1.00	25.17
	ATOM	863	N	GLY A 113	0	0.599	45.092	19.707	1.00	18.05
	ATOM	864	CA	GLY A 113	0	-0.554	44.236	19.433	1.00	19.69
	ATOM	865	C	GLY A 113	0	-0.085	42.819	19.096	1.00	22.25

	ATOM	866	O	GLY A 113	0	0.937	42.333	19.593	1.00	20.55
	ATOM	867	N	THR A 114	0	-0.817	42.173	18.186	1.00	20.91
	ATOM	868	CA	THR A 114	0	-0.493	40.816	17.749	1.00	20.85
	ATOM	869	C	THR A 114	0	0.296	40.774	16.471	1.00	18.04
5	ATOM	870	O	THR A 114	0	0.243	39.783	15.743	1.00	18.26
	ATOM	871	CB	THR A 114	0	-1.847	40.095	17.487	1.00	23.93
	ATOM	872	OG1	THR A 114	0	-2.609	40.910	16.554	1.00	25.68
	ATOM	873	CG2	THR A 114	0	-2.571	39.928	18.792	1.00	23.72
	ATOM	874	N	GLN A 115	0	1.023	41.819	16.095	1.00	17.04
10	ATOM	875	CA	GLN A 115	0	1.792	41.842	14.853	1.00	16.88
	ATOM	876	C	GLN A 115	0	2.881	40.775	14.744	1.00	17.94
	ATOM	877	O	GLN A 115	0	3.203	40.263	13.649	1.00	17.18
	ATOM	878	CB	GLN A 115	0	2.391	43.244	14.757	1.00	17.55
	ATOM	879	CG	GLN A 115	0	3.026	43.601	13.418	1.00	17.65
15	ATOM	880	CD	GLN A 115	0	3.558	45.024	13.418	1.00	17.73
	ATOM	881	OE1	GLN A 115	0	3.257	45.782	12.482	1.00	19.19
	ATOM	882	NE2	GLN A 115	0	4.334	45.421	14.422	1.00	14.70
	ATOM	883	N	TYR A 116	0	3.515	40.416	15.881	1.00	16.32
	ATOM	884	CA	TYR A 116	0	4.561	39.386	15.859	1.00	15.92
20	ATOM	885	C	TYR A 116	0	3.935	38.042	15.479	1.00	17.17
	ATOM	886	O	TYR A 116	0	4.584	37.258	14.786	1.00	16.70
	ATOM	887	CB	TYR A 116	0	5.411	39.312	17.096	1.00	13.45
	ATOM	888	CG	TYR A 116	0	5.209	38.487	18.314	1.00	10.97
	ATOM	889	CD1	TYR A 116	0	5.581	37.146	18.394	1.00	11.02
25	ATOM	890	CD2	TYR A 116	0	4.665	39.052	19.460	1.00	12.18
	ATOM	891	CE1	TYR A 116	0	5.364	36.399	19.532	1.00	10.02
	ATOM	892	CE2	TYR A 116	0	4.491	38.345	20.642	1.00	12.25
	ATOM	893	CZ	TYR A 116	0	4.838	36.996	20.649	1.00	11.73
	ATOM	894	OH	TYR A 116	0	4.642	36.295	21.821	1.00	12.72
30	ATOM	895	N	CYS A 117	0	2.654	37.829	15.842	1.00	17.70
	ATOM	896	CA	CYS A 117	0	1.965	36.617	15.424	1.00	18.01
	ATOM	897	C	CYS A 117	0	1.883	36.496	13.911	1.00	17.55
	ATOM	898	O	CYS A 117	0	1.796	35.352	13.450	1.00	17.50
	ATOM	899	CB	CYS A 117	0	0.565	36.528	16.042	1.00	17.90
35	ATOM	900	SG	CYS A 117	0	0.463	36.895	17.810	1.00	19.72
	ATOM	901	N	ASP A 118	0	2.001	37.568	13.136	1.00	15.51
	ATOM	902	CA	ASP A 118	0	1.953	37.509	11.696	1.00	17.74
	ATOM	903	C	ASP A 118	0	3.341	37.445	11.061	1.00	18.72

	ATOM	904	O	ASP A 118	0	3.494	37.770	9.865	1.00	17.47
	ATOM	905	CB	ASP A 118	0	1.142	38.696	11.131	1.00	18.61
	ATOM	906	CG	ASP A 118	0	-0.356	38.448	11.378	1.00	21.44
	ATOM	907	OD1	ASP A 118	0	-0.826	37.331	11.082	1.00	21.55
5	ATOM	908	OD2	ASP A 118	0	-1.064	39.333	11.885	1.00	21.54
	ATOM	909	N	GLY A 119	0	4.355	37.095	11.882	1.00	18.19
	ATOM	910	CA	GLY A 119	0	5.671	36.889	11.313	1.00	19.00
	ATOM	911	C	GLY A 119	0	6.751	37.898	11.590	1.00	19.79
	ATOM	912	O	GLY A 119	0	7.909	37.640	11.213	1.00	19.97
10	ATOM	913	N	LEU A 120	0	6.445	39.011	12.280	1.00	18.24
	ATOM	914	CA	LEU A 120	0	7.484	39.991	12.569	1.00	16.08
	ATOM	915	C	LEU A 120	0	8.210	39.565	13.848	1.00	16.53
	ATOM	916	O	LEU A 120	0	7.933	40.051	14.939	1.00	15.31
	ATOM	917	CB	LEU A 120	0	6.918	41.389	12.654	1.00	16.22
15	ATOM	918	CG	LEU A 120	0	7.916	42.540	12.830	1.00	17.73
	ATOM	919	CD1	LEU A 120	0	9.188	42.293	12.043	1.00	17.73
	ATOM	920	CD2	LEU A 120	0	7.302	43.880	12.448	1.00	16.66
	ATOM	921	N	ARG A 121	0	9.144	38.622	13.682	1.00	14.23
	ATOM	922	CA	ARG A 121	0	9.859	37.985	14.773	1.00	14.19
20	ATOM	923	C	ARG A 121	0	11.007	37.152	14.159	1.00	14.09
	ATOM	924	O	ARG A 121	0	10.936	36.787	12.978	1.00	13.72
	ATOM	925	CB	ARG A 121	0	8.934	37.061	15.581	1.00	12.30
	ATOM	926	CG	ARG A 121	0	8.253	35.999	14.728	1.00	12.44
	ATOM	927	CD	ARG A 121	0	7.303	35.098	15.518	1.00	11.94
25	ATOM	928	NE	ARG A 121	0	6.507	34.269	14.604	1.00	12.92
	ATOM	929	CZ	ARG A 121	0	5.413	33.570	14.933	1.00	10.55
	ATOM	930	NH1	ARG A 121	0	4.897	33.483	16.137	1.00	8.12
	ATOM	931	NH2	ARG A 121	0	4.803	32.946	13.930	1.00	10.40
	ATOM	932	N	GLY A 122	0	12.045	36.848	14.937	1.00	12.29
30	ATOM	933	CA	GLY A 122	0	13.162	36.078	14.364	1.00	11.42
	ATOM	934	C	GLY A 122	0	14.185	35.918	15.486	1.00	12.42
	ATOM	935	O	GLY A 122	0	14.095	36.604	16.509	1.00	11.47
	ATOM	936	N	PRO A 123	0	15.164	35.075	15.246	1.00	11.82
	ATOM	937	CA	PRO A 123	0	16.226	34.778	16.190	1.00	12.81
35	ATOM	938	C	PRO A 123	0	17.288	35.857	16.258	1.00	12.41
	ATOM	939	O	PRO A 123	0	17.565	36.580	15.302	1.00	12.03
	ATOM	940	CB	PRO A 123	0	16.833	33.416	15.713	1.00	12.34
	ATOM	941	CG	PRO A 123	0	16.567	33.494	14.223	1.00	12.19

	ATOM	942	CD	PRO	A	123	0	15.283	34.289	14.021	1.00	11.35
	ATOM	943	N	MET	A	124	0	17.903	36.027	17.431	1.00	14.30
	ATOM	944	CA	MET	A	124	0	18.959	37.024	17.628	1.00	14.19
	ATOM	945	C	MET	A	124	0	20.040	36.414	18.528	1.00	15.37
5	ATOM	946	O	MET	A	124	0	19.788	36.067	19.690	1.00	15.41
	ATOM	947	CB	MET	A	124	0	18.411	38.290	18.242	1.00	15.94
	ATOM	948	CG	MET	A	124	0	19.464	39.345	18.604	1.00	19.30
	ATOM	949	SD	MET	A	124	0	18.646	40.875	19.164	1.00	21.94
	ATOM	950	CE	MET	A	124	0	19.918	42.061	18.729	1.00	23.64
10	ATOM	951	N	VAL	A	125	0	21.212	36.178	17.939	1.00	13.74
	ATOM	952	CA	VAL	A	125	0	22.282	35.479	18.658	1.00	13.87
	ATOM	953	C	VAL	A	125	0	23.478	36.390	18.872	1.00	13.68
	ATOM	954	O	VAL	A	125	0	24.004	36.976	17.945	1.00	14.01
	ATOM	955	CB	VAL	A	125	0	22.672	34.139	18.005	1.00	12.58
15	ATOM	956	CG1	VAL	A	125	0	23.787	33.383	18.749	1.00	11.23
	ATOM	957	CG2	VAL	A	125	0	21.448	33.212	18.033	1.00	12.14
	ATOM	958	N	ILE	A	126	0	23.860	36.535	20.135	1.00	14.48
	ATOM	959	CA	ILE	A	126	0	25.016	37.295	20.557	1.00	14.53
	ATOM	960	C	ILE	A	126	0	26.131	36.348	21.054	1.00	13.58
20	ATOM	961	O	ILE	A	126	0	26.061	35.791	22.154	1.00	12.93
	ATOM	962	CB	ILE	A	126	0	24.649	38.295	21.662	1.00	14.95
	ATOM	963	CG1	ILE	A	126	0	23.563	39.302	21.254	1.00	15.29
	ATOM	964	CG2	ILE	A	126	0	25.901	39.014	22.174	1.00	14.24
	ATOM	965	CD1	ILE	A	126	0	23.703	39.905	19.896	1.00	15.84
25	ATOM	966	N	TYR	A	127	0	27.142	36.146	20.236	1.00	13.66
	ATOM	967	CA	TYR	A	127	0	28.278	35.258	20.529	1.00	14.62
	ATOM	968	C	TYR	A	127	0	29.328	35.778	21.507	1.00	15.97
	ATOM	969	O	TYR	A	127	0	29.626	36.977	21.669	1.00	15.27
	ATOM	970	CB	TYR	A	127	0	28.965	34.939	19.176	1.00	14.97
30	ATOM	971	CG	TYR	A	127	0	28.057	34.136	18.272	1.00	16.10
	ATOM	972	CD1	TYR	A	127	0	27.823	32.782	18.496	1.00	14.96
	ATOM	973	CD2	TYR	A	127	0	27.428	34.753	17.177	1.00	16.64
	ATOM	974	CE1	TYR	A	127	0	26.995	32.057	17.650	1.00	16.16
	ATOM	975	CE2	TYR	A	127	0	26.576	34.039	16.356	1.00	17.32
35	ATOM	976	CZ	TYR	A	127	0	26.374	32.692	16.592	1.00	18.16
	ATOM	977	OH	TYR	A	127	0	25.540	31.971	15.756	1.00	20.32
	ATOM	978	N	ASP	A	128	0	29.892	34.895	22.312	1.00	14.36
	ATOM	979	CA	ASP	A	128	0	30.825	35.269	23.365	1.00	16.80

	ATOM	980	C	ASP A 128	0	32.222	34.863	22.939	1.00	20.11
	ATOM	981	O	ASP A 128	0	32.508	33.656	22.777	1.00	21.41
	ATOM	982	CB	ASP A 128	0	30.398	34.568	24.649	1.00	16.65
	ATOM	983	CG	ASP A 128	0	31.136	35.055	25.874	1.00	18.36
5	ATOM	984	OD1	ASP A 128	0	32.194	35.708	25.750	1.00	18.72
	ATOM	985	OD2	ASP A 128	0	30.710	34.819	27.024	1.00	20.03
	ATOM	986	N	ASP A 129	0	33.148	35.798	22.771	1.00	22.30
	ATOM	987	CA	ASP A 129	0	34.511	35.389	22.377	1.00	24.39
	ATOM	988	C	ASP A 129	0	35.282	34.740	23.509	1.00	22.47
10	ATOM	989	O	ASP A 129	0	36.275	34.096	23.209	1.00	23.18
	ATOM	990	CB	ASP A 129	0	35.298	36.490	21.707	1.00	28.46
	ATOM	991	CG	ASP A 129	0	35.372	37.764	22.516	1.00	31.10
	ATOM	992	OD1	ASP A 129	0	35.254	37.652	23.747	1.00	32.87
	ATOM	993	OD2	ASP A 129	0	35.553	38.824	21.891	1.00	34.70
15	ATOM	994	N	ASN A 130	0	34.829	34.684	24.736	1.00	21.92
	ATOM	995	CA	ASN A 130	0	35.368	34.015	25.874	1.00	23.74
	ATOM	996	C	ASN A 130	0	34.382	32.976	26.417	1.00	23.02
	ATOM	997	O	ASN A 130	0	34.352	32.684	27.616	1.00	20.14
	ATOM	998	CB	ASN A 130	0	35.686	35.002	27.028	1.00	26.41
20	ATOM	999	CG	ASN A 130	0	36.583	36.127	26.550	1.00	30.99
	ATOM	1000	OD1	ASN A 130	0	36.187	37.309	26.486	1.00	33.20
	ATOM	1001	ND2	ASN A 130	0	37.818	35.769	26.175	1.00	30.96
	ATOM	1002	N	ASP A 131	0	33.533	32.401	25.561	1.00	23.32
	ATOM	1003	CA	ASP A 131	0	32.476	31.543	26.127	1.00	21.63
25	ATOM	1004	C	ASP A 131	0	33.010	30.514	27.103	1.00	19.56
	ATOM	1005	O	ASP A 131	0	33.704	29.569	26.766	1.00	19.71
	ATOM	1006	CB	ASP A 131	0	31.594	30.877	25.063	1.00	22.97
	ATOM	1007	CG	ASP A 131	0	30.220	30.487	25.591	1.00	24.48
	ATOM	1008	OD1	ASP A 131	0	30.181	29.525	26.397	1.00	26.42
30	ATOM	1009	OD2	ASP A 131	0	29.166	31.051	25.212	1.00	22.66
	ATOM	1010	N	PRO A 132	0	32.491	30.548	28.315	1.00	18.77
	ATOM	1011	CA	PRO A 132	0	32.759	29.611	29.381	1.00	19.41
	ATOM	1012	C	PRO A 132	0	32.523	28.141	29.031	1.00	20.89
	ATOM	1013	O	PRO A 132	0	33.112	27.250	29.672	1.00	19.99
35	ATOM	1014	CB	PRO A 132	0	31.799	29.990	30.531	1.00	18.42
	ATOM	1015	CG	PRO A 132	0	31.589	31.470	30.263	1.00	16.87
	ATOM	1016	CD	PRO A 132	0	31.645	31.673	28.778	1.00	16.73
	ATOM	1017	N	HIS A 133	0	31.668	27.836	28.063	1.00	19.47

	ATOM	1018	CA	HIS A 133	0	31.331	26.465	27.700	1.00	18.79
	ATOM	1019	C	HIS A 133	0	31.887	26.014	26.372	1.00	19.35
	ATOM	1020	O	HIS A 133	0	31.503	24.954	25.826	1.00	18.60
	ATOM	1021	CB	HIS A 133	0	29.789	26.428	27.536	1.00	18.91
5	ATOM	1022	CG	HIS A 133	0	29.065	26.242	28.815	1.00	18.13
	ATOM	1023	ND1	HIS A 133	0	29.566	25.551	29.877	1.00	19.52
	ATOM	1024	CD2	HIS A 133	0	27.817	26.625	29.183	1.00	19.38
	ATOM	1025	CE1	HIS A 133	0	28.679	25.530	30.855	1.00	20.08
	ATOM	1026	NE2	HIS A 133	0	27.587	26.180	30.457	1.00	19.60
10	ATOM	1027	N	ALA A 134	0	32.840	26.801	25.852	1.00	19.40
	ATOM	1028	CA	ALA A 134	0	33.413	26.465	24.552	1.00	21.88
	ATOM	1029	C	ALA A 134	0	34.080	25.107	24.525	1.00	21.69
	ATOM	1030	O	ALA A 134	0	34.120	24.514	23.439	1.00	21.61
	ATOM	1031	CB	ALA A 134	0	34.418	27.548	24.128	1.00	22.55
15	ATOM	1032	N	ALA A 135	0	34.582	24.527	25.622	1.00	21.96
	ATOM	1033	CA	ALA A 135	0	35.178	23.192	25.483	1.00	23.53
	ATOM	1034	C	ALA A 135	0	34.144	22.096	25.232	1.00	24.47
	ATOM	1035	O	ALA A 135	0	34.488	20.936	24.989	1.00	24.77
	ATOM	1036	CB	ALA A 135	0	35.910	22.820	26.776	1.00	21.92
20	ATOM	1037	N	LEU A 136	0	32.862	22.375	25.457	1.00	24.95
	ATOM	1038	CA	LEU A 136	0	31.800	21.376	25.404	1.00	23.15
	ATOM	1039	C	LEU A 136	0	31.284	21.076	24.016	1.00	20.31
	ATOM	1040	O	LEU A 136	0	30.609	20.054	23.924	1.00	19.62
	ATOM	1041	CB	LEU A 136	0	30.665	21.845	26.318	1.00	24.43
25	ATOM	1042	CG	LEU A 136	0	30.501	21.211	27.686	1.00	27.55
	ATOM	1043	CD1	LEU A 136	0	31.803	20.721	28.285	1.00	25.75
	ATOM	1044	CD2	LEU A 136	0	29.747	22.129	28.644	1.00	26.92
	ATOM	1045	N	TYR A 137	0	31.565	21.888	22.998	1.00	17.05
	ATOM	1046	CA	TYR A 137	0	31.085	21.612	21.662	1.00	16.65
30	ATOM	1047	C	TYR A 137	0	32.076	22.054	20.599	1.00	17.99
	ATOM	1048	O	TYR A 137	0	32.965	22.891	20.794	1.00	18.69
	ATOM	1049	CB	TYR A 137	0	29.724	22.319	21.402	1.00	16.73
	ATOM	1050	CG	TYR A 137	0	29.711	23.760	21.857	1.00	16.24
	ATOM	1051	CD1	TYR A 137	0	29.302	24.108	23.150	1.00	16.00
35	ATOM	1052	CD2	TYR A 137	0	30.159	24.754	21.001	1.00	14.76
	ATOM	1053	CE1	TYR A 137	0	29.355	25.448	23.551	1.00	15.32
	ATOM	1054	CE2	TYR A 137	0	30.165	26.081	21.396	1.00	15.52
	ATOM	1055	CZ	TYR A 137	0	29.759	26.410	22.675	1.00	15.61

ATOM 1056 OH TYR A 137 O 29.782 27.731 23.055 1.00 17.56
ATOM 1057 N ASP A 138 O 31.903 21.549 19.393 1.00 19.04
ATOM 1058 CA ASP A 138 O 32.733 21.859 18.253 1.00 20.02
ATOM 1059 C ASP A 138 O 32.139 22.933 17.364 1.00 21.05
5 ATOM 1060 O ASP A 138 O 32.911 23.553 16.631 1.00 21.98
ATOM 1061 CB ASP A 138 O 32.836 20.628 17.315 1.00 20.66
ATOM 1062 CG ASP A 138 O 33.355 19.455 18.089 1.00 22.79
ATOM 1063 OD1 ASP A 138 O 32.744 18.404 18.318 1.00 24.88
ATOM 1064 OD2 ASP A 138 O 34.481 19.675 18.581 1.00 25.34
10 ATOM 1065 N GLU A 139 O 30.825 22.957 17.184 1.00 19.73
ATOM 1066 CA GLU A 139 O 30.223 23.865 16.213 1.00 21.27
ATOM 1067 C GLU A 139 O 29.086 24.668 16.825 1.00 18.97
ATOM 1068 O GLU A 139 O 28.306 24.143 17.608 1.00 16.95
ATOM 1069 CB GLU A 139 O 29.617 23.164 15.000 1.00 24.71
15 ATOM 1070 CG GLU A 139 O 30.509 22.149 14.311 1.00 30.89
ATOM 1071 CD GLU A 139 O 31.633 22.868 13.587 1.00 34.42
ATOM 1072 OE1 GLU A 139 O 31.340 23.869 12.898 1.00 36.87
ATOM 1073 OE2 GLU A 139 O 32.794 22.457 13.705 1.00 37.60
ATOM 1074 N ASP A 140 O 29.057 25.933 16.408 1.00 19.38
20 ATOM 1075 CA ASP A 140 O 28.026 26.847 16.912 1.00 17.89
ATOM 1076 C ASP A 140 O 27.858 27.901 15.837 1.00 18.87
ATOM 1077 O ASP A 140 O 28.705 28.780 15.768 1.00 21.31
ATOM 1078 CB ASP A 140 O 28.438 27.399 18.268 1.00 16.26
ATOM 1079 CG ASP A 140 O 27.445 28.399 18.858 1.00 16.73
25 ATOM 1080 OD1 ASP A 140 O 27.854 29.143 19.781 1.00 14.86
ATOM 1081 OD2 ASP A 140 O 26.287 28.446 18.401 1.00 13.82
ATOM 1082 N ASP A 141 O 26.862 27.844 14.972 1.00 17.34
ATOM 1083 CA ASP A 141 O 26.750 28.859 13.937 1.00 19.52
ATOM 1084 C ASP A 141 O 25.301 29.031 13.520 1.00 19.33
30 ATOM 1085 O ASP A 141 O 24.342 28.513 14.115 1.00 17.91
ATOM 1086 CB ASP A 141 O 27.681 28.509 12.772 1.00 21.66
ATOM 1087 CG ASP A 141 O 27.384 27.151 12.193 1.00 24.87
ATOM 1088 OD1 ASP A 141 O 28.280 26.521 11.567 1.00 28.90
ATOM 1089 OD2 ASP A 141 O 26.271 26.604 12.302 1.00 25.89
35 ATOM 1090 N GLU A 142 O 25.102 29.688 12.387 1.00 19.21
ATOM 1091 CA GLU A 142 O 23.775 29.945 11.880 1.00 20.84
ATOM 1092 C GLU A 142 O 23.052 28.636 11.592 1.00 19.95
ATOM 1093 O GLU A 142 O 21.844 28.656 11.665 1.00 18.73

	ATOM	1094	CB	GLU	A 142	O	23.771	30.894	10.699	1.00	23.40
	ATOM	1095	CG	GLU	A 142	O	24.295	30.301	9.407	1.00	27.22
	ATOM	1096	CD	GLU	A 142	O	25.718	30.826	9.221	1.00	32.36
	ATOM	1097	OE1	GLU	A 142	O	26.513	30.920	10.206	1.00	31.87
5	ATOM	1098	OE2	GLU	A 142	O	25.968	31.136	8.023	1.00	35.76
	ATOM	1099	N	ASN	A 143	O	23.723	27.508	11.378	1.00	20.40
	ATOM	1100	CA	ASN	A 143	O	23.105	26.227	11.151	1.00	19.61
	ATOM	1101	C	ASN	A 143	O	22.785	25.468	12.421	1.00	18.35
	ATOM	1102	O	ASN	A 143	O	22.317	24.337	12.325	1.00	15.65
10	ATOM	1103	CB	ASN	A 143	O	24.024	25.401	10.229	1.00	23.57
	ATOM	1104	CG	ASN	A 143	O	24.133	26.067	8.857	1.00	26.63
	ATOM	1105	OD1	ASN	A 143	O	25.220	26.376	8.356	1.00	29.89
	ATOM	1106	ND2	ASN	A 143	O	23.049	26.342	8.175	1.00	25.46
	ATOM	1107	N	THR	A 144	O	23.067	25.974	13.632	1.00	16.76
15	ATOM	1108	CA	THR	A 144	O	22.678	25.257	14.825	1.00	15.40
	ATOM	1109	C	THR	A 144	O	21.556	25.976	15.577	1.00	15.58
	ATOM	1110	O	THR	A 144	O	21.361	25.776	16.789	1.00	17.88
	ATOM	1111	CB	THR	A 144	O	23.848	25.018	15.785	1.00	16.43
	ATOM	1112	OG1	THR	A 144	O	24.296	26.270	16.297	1.00	14.82
20	ATOM	1113	CG2	THR	A 144	O	24.935	24.215	15.104	1.00	15.98
	ATOM	1114	N	ILE	A 145	O	20.821	26.834	14.898	1.00	13.92
	ATOM	1115	CA	ILE	A 145	O	19.697	27.550	15.500	1.00	14.31
	ATOM	1116	C	ILE	A 145	O	18.392	26.835	15.139	1.00	13.84
	ATOM	1117	O	ILE	A 145	O	18.127	26.478	13.996	1.00	12.32
25	ATOM	1118	CB	ILE	A 145	O	19.641	29.016	15.011	1.00	15.15
	ATOM	1119	CG1	ILE	A 145	O	20.881	29.726	15.608	1.00	16.27
	ATOM	1120	CG2	ILE	A 145	O	18.346	29.736	15.375	1.00	13.14
	ATOM	1121	CD1	ILE	A 145	O	21.256	31.006	14.892	1.00	16.72
	ATOM	1122	N	ILE	A 146	O	17.550	26.644	16.141	1.00	13.54
30	ATOM	1123	CA	ILE	A 146	O	16.263	25.983	15.926	1.00	13.70
	ATOM	1124	C	ILE	A 146	O	15.167	26.899	16.494	1.00	12.67
	ATOM	1125	O	ILE	A 146	O	15.155	27.082	17.714	1.00	10.09
	ATOM	1126	CB	ILE	A 146	O	16.183	24.580	16.553	1.00	15.97
	ATOM	1127	CG1	ILE	A 146	O	17.280	23.621	16.012	1.00	17.29
35	ATOM	1128	CG2	ILE	A 146	O	14.831	23.937	16.207	1.00	14.52
	ATOM	1129	CD1	ILE	A 146	O	17.359	22.340	16.832	1.00	18.45
	ATOM	1130	N	THR	A 147	O	14.360	27.507	15.610	1.00	10.81
	ATOM	1131	CA	THR	A 147	O	13.240	28.310	16.102	1.00	12.54

ATOM 1132 C THR A 147 O 11.912 27.526 15.988 1.00 13.55
ATOM 1133 O THR A 147 O 11.655 26.724 15.076 1.00 12.65
ATOM 1134 CB THR A 147 O 13.078 29.642 15.351 1.00 12.37
ATOM 1135 OG1 THR A 147 O 12.728 29.311 14.005 1.00 10.17
5 ATOM 1136 CG2 THR A 147 O 14.381 30.479 15.402 1.00 11.93
ATOM 1137 N LEU A 148 O 11.062 27.715 16.972 1.00 12.48
ATOM 1138 CA LEU A 148 O 9.719 27.171 17.039 1.00 13.90
ATOM 1139 C LEU A 148 O 8.719 28.350 16.916 1.00 15.44
ATOM 1140 O LEU A 148 O 8.860 29.383 17.579 1.00 15.28
10 ATOM 1141 CB LEU A 148 O 9.501 26.419 18.340 1.00 12.83
ATOM 1142 CG LEU A 148 O 10.502 25.293 18.669 1.00 12.45
ATOM 1143 CD1 LEU A 148 O 10.154 24.669 19.997 1.00 11.49
ATOM 1144 CD2 LEU A 148 O 10.552 24.203 17.597 1.00 11.82
ATOM 1145 N ALA A 149 O 7.726 28.241 16.053 1.00 14.08
15 ATOM 1146 CA ALA A 149 O 6.725 29.256 15.825 1.00 15.37
ATOM 1147 C ALA A 149 O 5.336 28.658 15.521 1.00 16.78
ATOM 1148 O ALA A 149 O 5.198 27.637 14.841 1.00 15.78
ATOM 1149 CB ALA A 149 O 7.068 30.127 14.628 1.00 13.22
ATOM 1150 N ASP A 150 O 4.337 29.344 16.065 1.00 16.39
20 ATOM 1151 CA ASP A 150 O 2.941 28.995 15.864 1.00 15.96
ATOM 1152 C ASP A 150 O 2.515 29.758 14.624 1.00 16.53
ATOM 1153 O ASP A 150 O 2.960 30.905 14.483 1.00 18.17
ATOM 1154 CB ASP A 150 O 2.066 29.440 17.027 1.00 16.78
ATOM 1155 CG ASP A 150 O 2.345 30.836 17.561 1.00 18.15
25 ATOM 1156 OD1 ASP A 150 O 3.410 31.472 17.347 1.00 16.29
ATOM 1157 OD2 ASP A 150 O 1.414 31.311 18.264 1.00 17.83
ATOM 1158 N TRP A 151 O 1.776 29.157 13.726 1.00 15.62
ATOM 1159 CA TRP A 151 O 1.366 29.828 12.499 1.00 14.37
ATOM 1160 C TRP A 151 O -0.140 29.688 12.226 1.00 14.78
30 ATOM 1161 O TRP A 151 O -0.679 28.607 12.425 1.00 13.41
ATOM 1162 CB TRP A 151 O 2.229 29.239 11.373 1.00 13.56
ATOM 1163 CG TRP A 151 O 2.046 30.004 10.097 1.00 13.31
ATOM 1164 CD1 TRP A 151 O 1.385 29.545 8.991 1.00 13.60
ATOM 1165 CD2 TRP A 151 O 2.484 31.316 9.806 1.00 15.46
35 ATOM 1166 NE1 TRP A 151 O 1.412 30.497 8.017 1.00 14.49
ATOM 1167 CE2 TRP A 151 O 2.061 31.605 8.473 1.00 15.53
ATOM 1168 CE3 TRP A 151 O 3.189 32.294 10.522 1.00 16.28
ATOM 1169 CZ2 TRP A 151 O 2.306 32.822 7.846 1.00 16.57

ATOM 1170 CZ3 TRP A 151 O 3.436 33.505 9.881 1.00 18.22
ATOM 1171 CH2 TRP A 151 O 3.003 33.766 8.560 1.00 18.00
ATOM 1172 N TYR A 152 O -0.818 30.745 11.812 1.00 15.59
ATOM 1173 CA TYR A 152 O -2.266 30.813 11.614 1.00 17.47
5 ATOM 1174 C TYR A 152 O -2.556 31.086 10.149 1.00 18.79
ATOM 1175 O TYR A 152 O -1.830 31.856 9.521 1.00 19.15
ATOM 1176 CB TYR A 152 O -2.981 31.930 12.434 1.00 16.37
ATOM 1177 CG TYR A 152 O -2.539 31.776 13.887 1.00 16.24
ATOM 1178 CD1 TYR A 152 O -1.313 32.303 14.318 1.00 15.22
10 ATOM 1179 CD2 TYR A 152 O -3.267 30.998 14.767 1.00 15.29
ATOM 1180 CE1 TYR A 152 O -0.889 32.135 15.626 1.00 14.67
ATOM 1181 CE2 TYR A 152 O -2.831 30.799 16.054 1.00 16.52
ATOM 1182 CZ TYR A 152 O -1.632 31.369 16.474 1.00 16.12
ATOM 1183 OH TYR A 152 O -1.219 31.139 17.771 1.00 16.36
15 ATOM 1184 N HIS A 153 O -3.590 30.445 9.599 1.00 20.39
ATOM 1185 CA HIS A 153 O -3.899 30.683 8.181 1.00 21.90
ATOM 1186 C HIS A 153 O -4.642 31.988 7.952 1.00 21.94
ATOM 1187 O HIS A 153 O -4.750 32.386 6.784 1.00 22.32
ATOM 1188 CB HIS A 153 O -4.592 29.483 7.549 1.00 22.29
20 ATOM 1189 CG HIS A 153 O -3.651 28.319 7.385 1.00 24.52
ATOM 1190 ND1 HIS A 153 O -4.071 27.022 7.258 1.00 24.25
ATOM 1191 CD2 HIS A 153 O -2.286 28.274 7.338 1.00 23.32
ATOM 1192 CE1 HIS A 153 O -3.034 26.220 7.124 1.00 24.15
ATOM 1193 NE2 HIS A 153 O -1.956 26.965 7.178 1.00 24.30
25 ATOM 1194 N ILE A 154 O -5.084 32.718 8.972 1.00 21.86
ATOM 1195 CA ILE A 154 O -5.611 34.046 8.686 1.00 24.39
ATOM 1196 C ILE A 154 O -4.904 35.051 9.597 1.00 22.15
ATOM 1197 O ILE A 154 O -4.517 34.732 10.698 1.00 20.15
ATOM 1198 CB ILE A 154 O -7.120 34.281 8.693 1.00 26.43
30 ATOM 1199 CG1 ILE A 154 O -7.682 34.498 10.099 1.00 27.66
ATOM 1200 CG2 ILE A 154 O -7.947 33.251 7.928 1.00 26.60
ATOM 1201 CD1 ILE A 154 O -7.312 33.468 11.125 1.00 28.86
ATOM 1202 N PRO A 155 O -4.723 36.255 9.105 1.00 23.79
ATOM 1203 CA PRO A 155 O -4.108 37.361 9.816 1.00 23.66
35 ATOM 1204 C PRO A 155 O -4.604 37.435 11.252 1.00 24.59
ATOM 1205 O PRO A 155 O -5.814 37.317 11.539 1.00 24.53
ATOM 1206 CB PRO A 155 O -4.546 38.634 9.077 1.00 24.20
ATOM 1207 CG PRO A 155 O -4.990 38.162 7.733 1.00 23.40

ATOM 1208 CD PRO A 155 0 -5.207 36.672 7.776 1.00 23.41
ATOM 1209 N ALA A 156 0 -3.704 37.776 12.178 1.00 24.03
ATOM 1210 CA ALA A 156 0 -4.066 37.806 13.588 1.00 25.45
ATOM 1211 C ALA A 156 0 -5.262 38.667 13.992 1.00 24.85
5 ATOM 1212 O ALA A 156 0 -6.083 38.217 14.798 1.00 22.79
ATOM 1213 CB ALA A 156 0 -2.866 38.045 14.492 1.00 24.30
ATOM 1214 N PRO A 157 0 -5.393 39.873 13.518 1.00 25.98
ATOM 1215 CA PRO A 157 0 -6.521 40.741 13.807 1.00 28.77
ATOM 1216 C PRO A 157 0 -7.840 40.092 13.406 1.00 30.78
10 ATOM 1217 O PRO A 157 0 -8.798 40.416 14.105 1.00 34.62
ATOM 1218 CB PRO A 157 0 -6.324 42.071 13.068 1.00 26.56
ATOM 1219 CG PRO A 157 0 -4.859 42.013 12.762 1.00 25.98
ATOM 1220 CD PRO A 157 0 -4.480 40.547 12.585 1.00 25.96
ATOM 1221 N SER A 158 0 -7.950 39.207 12.430 1.00 30.95
15 ATOM 1222 CA SER A 158 0 -9.174 38.549 12.047 1.00 31.32
ATOM 1223 C SER A 158 0 -9.450 37.288 12.851 1.00 33.61
ATOM 1224 O SER A 158 0 -10.472 36.633 12.575 1.00 34.71
ATOM 1225 CB SER A 158 0 -9.176 38.118 10.577 1.00 30.14
ATOM 1226 OG SER A 158 0 -8.942 39.187 9.665 1.00 31.20
20 ATOM 1227 N ILE A 159 0 -8.588 36.875 13.773 1.00 34.23
ATOM 1228 CA ILE A 159 0 -8.918 35.642 14.491 1.00 36.40
ATOM 1229 C ILE A 159 0 -10.189 35.896 15.309 1.00 39.20
ATOM 1230 O ILE A 159 0 -10.294 36.875 16.046 1.00 39.00
ATOM 1231 CB ILE A 159 0 -7.769 35.121 15.360 1.00 35.56
25 ATOM 1232 CG1 ILE A 159 0 -6.713 34.408 14.485 1.00 35.58
ATOM 1233 CG2 ILE A 159 0 -8.262 34.184 16.452 1.00 34.97
ATOM 1234 CD1 ILE A 159 0 -5.388 34.268 15.212 1.00 34.91
ATOM 1235 N GLN A 160 0 -11.137 34.969 15.196 1.00 41.53
ATOM 1236 CA GLN A 160 0 -12.398 35.056 15.946 1.00 42.57
30 ATOM 1237 C GLN A 160 0 -12.466 33.914 16.949 1.00 40.51
ATOM 1238 O GLN A 160 0 -12.308 32.741 16.585 1.00 41.96
ATOM 1239 CB GLN A 160 0 -13.542 35.062 14.937 1.00 45.52
ATOM 1240 CG GLN A 160 0 -14.814 34.319 15.267 1.00 48.48
ATOM 1241 CD GLN A 160 0 -15.570 33.799 14.055 1.00 50.12
35 ATOM 1242 OE1 GLN A 160 0 -16.204 32.737 14.118 1.00 50.77
ATOM 1243 NE2 GLN A 160 0 -15.504 34.520 12.940 1.00 51.22
ATOM 1244 N GLY A 161 0 -12.667 34.191 18.225 1.00 37.10
ATOM 1245 CA GLY A 161 0 -12.722 33.112 19.208 1.00 34.91

	ATOM	1246	C	GLY A 161	0	-11.305	32.826	19.696	1.00	34.13
	ATOM	1247	O	GLY A 161	0	-10.412	33.648	19.451	1.00	32.40
	ATOM	1248	N	ALA A 162	0	-11.158	31.738	20.433	1.00	33.01
	ATOM	1249	CA	ALA A 162	0	-9.864	31.355	20.988	1.00	32.39
5	ATOM	1250	C	ALA A 162	0	-8.927	30.902	19.880	1.00	31.53
	ATOM	1251	O	ALA A 162	0	-9.285	30.132	19.013	1.00	30.73
	ATOM	1252	CB	ALA A 162	0	-10.058	30.263	22.010	1.00	34.12
	ATOM	1253	N	ALA A 163	0	-7.731	31.475	19.851	1.00	32.06
	ATOM	1254	CA	ALA A 163	0	-6.740	31.202	18.814	1.00	30.85
10	ATOM	1255	C	ALA A 163	0	-6.219	29.774	18.897	1.00	29.40
	ATOM	1256	O	ALA A 163	0	-5.967	29.223	19.965	1.00	30.49
	ATOM	1257	CB	ALA A 163	0	-5.607	32.217	18.911	1.00	30.29
	ATOM	1258	N	GLN A 164	0	-6.101	29.130	17.754	1.00	28.69
	ATOM	1259	CA	GLN A 164	0	-5.616	27.769	17.612	1.00	28.24
15	ATOM	1260	C	GLN A 164	0	-4.720	27.744	16.370	1.00	25.02
	ATOM	1261	O	GLN A 164	0	-5.157	28.046	15.260	1.00	23.64
	ATOM	1262	CB	GLN A 164	0	-6.732	26.756	17.361	1.00	31.99
	ATOM	1263	CG	GLN A 164	0	-7.885	26.640	18.319	1.00	36.24
	ATOM	1264	CD	GLN A 164	0	-7.535	25.809	19.540	1.00	40.95
20	ATOM	1265	OE1	GLN A 164	0	-7.863	26.166	20.684	1.00	43.34
	ATOM	1266	NE2	GLN A 164	0	-6.864	24.672	19.328	1.00	41.86
	ATOM	1267	N	PRO A 165	0	-3.446	27.406	16.549	1.00	22.68
	ATOM	1268	CA	PRO A 165	0	-2.501	27.360	15.463	1.00	20.43
	ATOM	1269	C	PRO A 165	0	-2.856	26.294	14.429	1.00	18.89
25	ATOM	1270	O	PRO A 165	0	-3.286	25.176	14.715	1.00	18.00
	ATOM	1271	CB	PRO A 165	0	-1.126	27.075	16.088	1.00	20.83
	ATOM	1272	CG	PRO A 165	0	-1.476	26.651	17.479	1.00	22.05
	ATOM	1273	CD	PRO A 165	0	-2.873	27.081	17.851	1.00	21.57
	ATOM	1274	N	ASP A 166	0	-2.667	26.608	13.169	1.00	17.50
30	ATOM	1275	CA	ASP A 166	0	-2.829	25.677	12.059	1.00	19.82
	ATOM	1276	C	ASP A 166	0	-1.591	24.788	11.930	1.00	19.47
	ATOM	1277	O	ASP A 166	0	-1.692	23.649	11.506	1.00	19.38
	ATOM	1278	CB	ASP A 166	0	-3.005	26.413	10.727	1.00	19.75
	ATOM	1279	CG	ASP A 166	0	-4.347	27.162	10.728	1.00	21.69
35	ATOM	1280	OD1	ASP A 166	0	-5.376	26.480	10.593	1.00	22.24
	ATOM	1281	OD2	ASP A 166	0	-4.384	28.392	10.885	1.00	22.13
	ATOM	1282	N	ALA A 167	0	-0.435	25.386	12.231	1.00	18.54
	ATOM	1283	CA	ALA A 167	0	0.806	24.614	12.142	1.00	18.74

	ATOM	1284	C	ALA A 167	0	1.867	25.056	13.148	1.00	17.69
	ATOM	1285	O	ALA A 167	0	1.874	26.147	13.715	1.00	15.83
	ATOM	1286	CB	ALA A 167	0	1.387	24.767	10.735	1.00	17.32
	ATOM	1287	N	THR A 168	0	2.826	24.166	13.335	1.00	18.40
5	ATOM	1288	CA	THR A 168	0	4.087	24.402	14.027	1.00	14.85
	ATOM	1289	C	THR A 168	0	5.180	24.553	12.955	1.00	15.24
	ATOM	1290	O	THR A 168	0	5.402	23.737	12.071	1.00	12.99
	ATOM	1291	CB	THR A 168	0	4.530	23.235	14.900	1.00	14.31
	ATOM	1292	OG1	THR A 168	0	3.558	23.068	15.920	1.00	12.30
10	ATOM	1293	CG2	THR A 168	0	5.921	23.516	15.524	1.00	13.60
	ATOM	1294	N	LEU A 169	0	5.867	25.686	12.973	1.00	16.69
	ATOM	1295	CA	LEU A 169	0	6.976	26.002	12.071	1.00	14.74
	ATOM	1296	C	LEU A 169	0	8.285	25.747	12.833	1.00	14.34
	ATOM	1297	O	LEU A 169	0	8.497	26.259	13.942	1.00	12.34
15	ATOM	1298	CB	LEU A 169	0	6.890	27.471	11.652	1.00	14.90
	ATOM	1299	CG	LEU A 169	0	6.071	27.845	10.428	1.00	17.83
	ATOM	1300	CD1	LEU A 169	0	4.978	26.825	10.133	1.00	15.89
	ATOM	1301	CD2	LEU A 169	0	5.500	29.254	10.443	1.00	16.43
	ATOM	1302	N	ILE A 170	0	9.141	24.923	12.255	1.00	14.06
20	ATOM	1303	CA	ILE A 170	0	10.472	24.659	12.819	1.00	14.01
	ATOM	1304	C	ILE A 170	0	11.397	25.312	11.784	1.00	15.19
	ATOM	1305	O	ILE A 170	0	11.307	25.009	10.585	1.00	14.73
	ATOM	1306	CB	ILE A 170	0	10.807	23.179	13.025	1.00	14.75
	ATOM	1307	CG1	ILE A 170	0	9.849	22.605	14.069	1.00	13.74
25	ATOM	1308	CG2	ILE A 170	0	12.268	22.983	13.468	1.00	13.47
	ATOM	1309	CD1	ILE A 170	0	9.915	21.134	14.385	1.00	15.26
	ATOM	1310	N	ASN A 171	0	12.166	26.317	12.208	1.00	13.13
	ATOM	1311	CA	ASN A 171	0	12.992	27.042	11.250	1.00	13.74
	ATOM	1312	C	ASN A 171	0	12.163	27.517	10.083	1.00	13.71
30	ATOM	1313	O	ASN A 171	0	12.562	27.381	8.921	1.00	13.20
	ATOM	1314	CB	ASN A 171	0	14.220	26.209	10.793	1.00	14.42
	ATOM	1315	CG	ASN A 171	0	15.236	26.157	11.940	1.00	16.29
	ATOM	1316	OD1	ASN A 171	0	15.123	26.983	12.875	1.00	16.78
	ATOM	1317	ND2	ASN A 171	0	16.203	25.259	11.964	1.00	14.32
35	ATOM	1318	N	GLY A 172	0	10.967	28.074	10.337	1.00	14.17
	ATOM	1319	CA	GLY A 172	0	10.157	28.619	9.270	1.00	11.74
	ATOM	1320	C	GLY A 172	0	9.387	27.636	8.433	1.00	14.40
	ATOM	1321	O	GLY A 172	0	8.783	28.064	7.441	1.00	15.60

	ATOM	1322	N	LYS A 173	0	9.430	26.319	8.669	1.00	13.84
	ATOM	1323	CA	LYS A 173	0	8.777	25.363	7.794	1.00	13.67
	ATOM	1324	C	LYS A 173	0	8.038	24.303	8.589	1.00	13.59
	ATOM	1325	O	LYS A 173	0	8.445	24.027	9.723	1.00	11.70
5	ATOM	1326	CB	LYS A 173	0	9.775	24.645	6.875	1.00	17.03
	ATOM	1327	CG	LYS A 173	0	10.704	25.577	6.118	1.00	17.63
	ATOM	1328	CD	LYS A 173	0	11.508	24.796	5.094	1.00	20.84
	ATOM	1329	CE	LYS A 173	0	12.213	25.821	4.198	1.00	22.63
	ATOM	1330	NZ	LYS A 173	0	13.304	25.087	3.499	1.00	28.08
10	ATOM	1331	N	GLY A 174	0	6.922	23.821	8.014	1.00	12.28
	ATOM	1332	CA	GLY A 174	0	6.178	22.768	8.753	1.00	11.45
	ATOM	1333	C	GLY A 174	0	4.958	22.409	7.896	1.00	13.55
	ATOM	1334	O	GLY A 174	0	4.823	22.877	6.760	1.00	13.37
	ATOM	1335	N	ARG A 175	0	4.042	21.619	8.432	1.00	14.54
15	ATOM	1336	CA	ARG A 175	0	2.859	21.201	7.687	1.00	16.62
	ATOM	1337	C	ARG A 175	0	1.598	21.336	8.541	1.00	17.67
	ATOM	1338	O	ARG A 175	0	1.727	21.264	9.769	1.00	18.41
	ATOM	1339	CB	ARG A 175	0	2.985	19.718	7.292	1.00	16.05
	ATOM	1340	CG	ARG A 175	0	3.894	19.472	6.116	1.00	16.55
20	ATOM	1341	CD	ARG A 175	0	4.358	18.009	6.108	1.00	17.70
	ATOM	1342	NE	ARG A 175	0	5.421	17.861	5.097	1.00	17.74
	ATOM	1343	CZ	ARG A 175	0	5.971	16.667	4.792	1.00	17.63
	ATOM	1344	NH1	ARG A 175	0	6.918	16.665	3.866	1.00	17.25
	ATOM	1345	NH2	ARG A 175	0	5.594	15.538	5.375	1.00	14.80
25	ATOM	1346	N	TYR A 176	0	0.429	21.438	7.908	1.00	18.08
	ATOM	1347	CA	TYR A 176	0	-0.800	21.481	8.746	1.00	18.67
	ATOM	1348	C	TYR A 176	0	-1.613	20.200	8.509	1.00	18.24
	ATOM	1349	O	TYR A 176	0	-1.417	19.534	7.483	1.00	17.67
	ATOM	1350	CB	TYR A 176	0	-1.635	22.709	8.462	1.00	17.21
30	ATOM	1351	CG	TYR A 176	0	-2.102	22.931	7.053	1.00	16.36
	ATOM	1352	CD1	TYR A 176	0	-1.246	23.433	6.089	1.00	14.84
	ATOM	1353	CD2	TYR A 176	0	-3.441	22.676	6.677	1.00	17.26
	ATOM	1354	CE1	TYR A 176	0	-1.640	23.686	4.796	1.00	16.01
	ATOM	1355	CE2	TYR A 176	0	-3.862	22.908	5.361	1.00	16.65
35	ATOM	1356	CZ	TYR A 176	0	-2.967	23.407	4.432	1.00	17.65
	ATOM	1357	OH	TYR A 176	0	-3.347	23.678	3.131	1.00	17.81
	ATOM	1358	N	VAL A 177	0	-2.427	19.815	9.464	1.00	18.46
	ATOM	1359	CA	VAL A 177	0	-3.200	18.571	9.303	1.00	21.18

	ATOM	1360	C	VAL A 177	0	-4.090	18.639	8.073	1.00	21.50
	ATOM	1361	O	VAL A 177	0	-4.788	19.620	7.858	1.00	21.85
	ATOM	1362	CB	VAL A 177	0	-4.072	18.306	10.532	1.00	22.29
	ATOM	1363	CG1	VAL A 177	0	-4.802	16.974	10.370	1.00	21.70
5	ATOM	1364	CG2	VAL A 177	0	-3.205	18.289	11.784	1.00	22.43
	ATOM	1365	N	GLY A 178	0	-3.989	17.707	7.142	1.00	21.84
	ATOM	1366	CA	GLY A 178	0	-4.761	17.742	5.918	1.00	20.35
	ATOM	1367	C	GLY A 178	0	-4.047	18.602	4.900	1.00	22.84
	ATOM	1368	O	GLY A 178	0	-4.576	18.673	3.774	1.00	23.86
10	ATOM	1369	N	GLY A 179	0	-2.887	19.220	5.210	1.00	21.49
	ATOM	1370	CA	GLY A 179	0	-2.291	20.060	4.149	1.00	19.94
	ATOM	1371	C	GLY A 179	0	-1.389	19.250	3.242	1.00	18.86
	ATOM	1372	O	GLY A 179	0	-1.192	18.052	3.399	1.00	19.35
	ATOM	1373	N	PRO A 180	0	-0.800	19.905	2.268	1.00	19.42
15	ATOM	1374	CA	PRO A 180	0	0.150	19.328	1.335	1.00	19.92
	ATOM	1375	C	PRO A 180	0	1.430	18.922	2.041	1.00	20.56
	ATOM	1376	O	PRO A 180	0	1.731	19.399	3.145	1.00	20.66
	ATOM	1377	CB	PRO A 180	0	0.503	20.399	0.298	1.00	19.52
	ATOM	1378	CG	PRO A 180	0	-0.144	21.639	0.829	1.00	19.70
20	ATOM	1379	CD	PRO A 180	0	-0.930	21.356	2.081	1.00	19.79
	ATOM	1380	N	ALA A 181	0	2.213	18.059	1.403	1.00	21.19
	ATOM	1381	CA	ALA A 181	0	3.489	17.644	2.007	1.00	23.04
	ATOM	1382	C	ALA A 181	0	4.548	18.723	1.772	1.00	21.24
	ATOM	1383	O	ALA A 181	0	5.465	18.522	0.986	1.00	23.93
25	ATOM	1384	CB	ALA A 181	0	3.928	16.305	1.435	1.00	21.73
	ATOM	1385	N	ALA A 182	0	4.398	19.905	2.315	1.00	19.30
	ATOM	1386	CA	ALA A 182	0	5.357	20.987	2.183	1.00	18.39
	ATOM	1387	C	ALA A 182	0	6.706	20.549	2.791	1.00	17.36
	ATOM	1388	O	ALA A 182	0	6.858	19.712	3.701	1.00	16.16
30	ATOM	1389	CB	ALA A 182	0	4.826	22.209	2.932	1.00	17.68
	ATOM	1390	N	GLU A 183	0	7.739	21.103	2.210	1.00	18.23
	ATOM	1391	CA	GLU A 183	0	9.134	20.882	2.599	1.00	20.90
	ATOM	1392	C	GLU A 183	0	9.381	21.078	4.093	1.00	18.87
	ATOM	1393	O	GLU A 183	0	8.976	22.073	4.699	1.00	17.80
35	ATOM	1394	CB	GLU A 183	0	9.990	21.875	1.820	1.00	25.16
	ATOM	1395	CG	GLU A 183	0	11.508	21.760	1.962	1.00	31.31
	ATOM	1396	CD	GLU A 183	0	12.075	22.803	0.998	1.00	34.38
	ATOM	1397	OE1	GLU A 183	0	11.901	22.609	-0.229	1.00	36.88

ATOM 1398 OE2 GLU A 183 O 12.619 23.809 1.484 1.00 36.18
ATOM 1399 N LEU A 184 O 10.010 20.093 4.691 1.00 17.33
ATOM 1400 CA LEU A 184 O 10.388 20.155 6.098 1.00 18.77
ATOM 1401 C LEU A 184 O 11.780 20.743 6.255 1.00 19.44
5 ATOM 1402 O LEU A 184 O 12.582 20.687 5.314 1.00 20.95
ATOM 1403 CB LEU A 184 O 10.331 18.735 6.673 1.00 18.11
ATOM 1404 CG LEU A 184 O 8.915 18.125 6.577 1.00 19.10
ATOM 1405 CD1 LEU A 184 O 8.887 16.734 7.178 1.00 18.87
ATOM 1406 CD2 LEU A 184 O 7.868 19.026 7.229 1.00 18.69
10 ATOM 1407 N SER A 185 O 12.054 21.342 7.398 1.00 18.46
ATOM 1408 CA SER A 185 O 13.366 21.883 7.699 1.00 17.73
ATOM 1409 C SER A 185 O 14.298 20.699 8.018 1.00 16.95
ATOM 1410 O SER A 185 O 13.883 19.710 8.629 1.00 15.84
ATOM 1411 CB SER A 185 O 13.303 22.786 8.934 1.00 17.34
15 ATOM 1412 OG SER A 185 O 12.846 24.073 8.560 1.00 18.09
ATOM 1413 N ILE A 186 O 15.533 20.845 7.587 1.00 16.43
ATOM 1414 CA ILE A 186 O 16.595 19.858 7.821 1.00 16.85
ATOM 1415 C ILE A 186 O 17.725 20.491 8.626 1.00 15.86
ATOM 1416 O ILE A 186 O 18.178 21.605 8.387 1.00 11.67
20 ATOM 1417 CB ILE A 186 O 17.193 19.390 6.471 1.00 18.77
ATOM 1418 CG1 ILE A 186 O 16.048 18.895 5.557 1.00 19.78
ATOM 1419 CG2 ILE A 186 O 18.167 18.241 6.697 1.00 18.53
ATOM 1420 CD1 ILE A 186 O 16.464 18.731 4.110 1.00 22.35
ATOM 1421 N VAL A 187 O 18.114 19.840 9.703 1.00 16.18
25 ATOM 1422 CA VAL A 187 O 19.243 20.287 10.505 1.00 16.63
ATOM 1423 C VAL A 187 O 20.362 19.239 10.231 1.00 17.36
ATOM 1424 O VAL A 187 O 20.158 18.046 10.505 1.00 15.19
ATOM 1425 CB VAL A 187 O 18.928 20.323 11.984 1.00 16.68
ATOM 1426 CG1 VAL A 187 O 20.198 20.622 12.796 1.00 16.82
30 ATOM 1427 CG2 VAL A 187 O 17.874 21.375 12.275 1.00 17.07
ATOM 1428 N ASN A 188 O 21.449 19.695 9.634 1.00 16.45
ATOM 1429 CA ASN A 188 O 22.528 18.766 9.272 1.00 19.84
ATOM 1430 C ASN A 188 O 23.598 18.597 10.349 1.00 19.41
ATOM 1431 O ASN A 188 O 24.051 19.618 10.862 1.00 21.31
35 ATOM 1432 CB ASN A 188 O 23.209 19.246 7.976 1.00 18.78
ATOM 1433 CG ASN A 188 O 22.249 19.186 6.797 1.00 20.77
ATOM 1434 OD1 ASN A 188 O 21.734 20.201 6.305 1.00 21.70
ATOM 1435 ND2 ASN A 188 O 21.995 17.985 6.286 1.00 20.52

	ATOM	1436	N	VAL A 189	0	24.024	17.389	10.681	1.00	17.35
	ATOM	1437	CA	VAL A 189	0	25.098	17.164	11.617	1.00	17.93
	ATOM	1438	C	VAL A 189	0	26.091	16.135	11.046	1.00	19.82
	ATOM	1439	O	VAL A 189	0	25.773	15.392	10.109	1.00	18.90
5	ATOM	1440	CB	VAL A 189	0	24.660	16.684	13.009	1.00	18.43
	ATOM	1441	CG1	VAL A 189	0	23.931	17.796	13.766	1.00	18.89
	ATOM	1442	CG2	VAL A 189	0	23.760	15.449	12.965	1.00	15.94
	ATOM	1443	N	GLU A 190	0	27.242	15.993	11.688	1.00	21.48
	ATOM	1444	CA	GLU A 190	0	28.220	14.972	11.274	1.00	24.63
10	ATOM	1445	C	GLU A 190	0	28.514	14.065	12.469	1.00	23.06
	ATOM	1446	O	GLU A 190	0	28.797	14.650	13.522	1.00	21.04
	ATOM	1447	CB	GLU A 190	0	29.569	15.551	10.860	1.00	26.79
	ATOM	1448	CG	GLU A 190	0	29.571	16.355	9.567	1.00	32.24
	ATOM	1449	CD	GLU A 190	0	30.951	16.990	9.351	1.00	34.67
15	ATOM	1450	OE1	GLU A 190	0	31.927	16.199	9.305	1.00	35.41
	ATOM	1451	OE2	GLU A 190	0	30.999	18.236	9.264	1.00	35.78
	ATOM	1452	N	GLN A 191	0	28.490	12.752	12.256	1.00	21.94
	ATOM	1453	CA	GLN A 191	0	28.768	11.824	13.357	1.00	21.92
	ATOM	1454	C	GLN A 191	0	30.121	12.151	13.984	1.00	22.68
20	ATOM	1455	O	GLN A 191	0	31.052	12.516	13.251	1.00	23.08
	ATOM	1456	CB	GLN A 191	0	28.797	10.400	12.820	1.00	22.01
	ATOM	1457	CG	GLN A 191	0	28.795	9.347	13.917	1.00	23.87
	ATOM	1458	CD	GLN A 191	0	28.846	7.966	13.259	1.00	26.64
	ATOM	1459	OE1	GLN A 191	0	29.745	7.761	12.427	1.00	28.86
25	ATOM	1460	NE2	GLN A 191	0	27.909	7.080	13.563	1.00	26.40
	ATOM	1461	N	GLY A 192	0	30.224	12.119	15.290	1.00	21.84
	ATOM	1462	CA	GLY A 192	0	31.418	12.469	15.996	1.00	22.91
	ATOM	1463	C	GLY A 192	0	31.564	13.910	16.446	1.00	23.87
	ATOM	1464	O	GLY A 192	0	32.394	14.174	17.322	1.00	25.80
30	ATOM	1465	N	LYS A 193	0	30.839	14.867	15.922	1.00	23.54
	ATOM	1466	CA	LYS A 193	0	30.899	16.259	16.362	1.00	22.84
	ATOM	1467	C	LYS A 193	0	29.840	16.584	17.404	1.00	21.67
	ATOM	1468	O	LYS A 193	0	28.826	15.882	17.538	1.00	20.99
	ATOM	1469	CB	LYS A 193	0	30.682	17.155	15.143	1.00	24.53
35	ATOM	1470	CG	LYS A 193	0	31.900	17.149	14.217	1.00	27.82
	ATOM	1471	CD	LYS A 193	0	31.739	18.261	13.199	1.00	30.02
	ATOM	1472	CE	LYS A 193	0	33.060	19.001	12.990	1.00	31.93
	ATOM	1473	NZ	LYS A 193	0	33.392	18.906	11.540	1.00	33.14

ATOM 1474 N LYS A 194 0 30.067 17.626 18.169 1.00 19.25
ATOM 1475 CA LYS A 194 0 29.168 18.115 19.187 1.00 19.49
ATOM 1476 C LYS A 194 0 28.722 19.523 18.780 1.00 19.40
ATOM 1477 O LYS A 194 0 29.512 20.285 18.235 1.00 19.29
5 ATOM 1478 CB LYS A 194 0 29.771 18.115 20.576 1.00 21.88
ATOM 1479 CG LYS A 194 0 30.338 16.748 20.999 1.00 25.59
ATOM 1480 CD LYS A 194 0 31.054 16.902 22.331 1.00 29.48
ATOM 1481 CE LYS A 194 0 31.455 15.582 22.970 1.00 33.58
ATOM 1482 NZ LYS A 194 0 30.363 15.049 23.868 1.00 35.93
10 ATOM 1483 N TYR A 195 0 27.418 19.818 18.910 1.00 16.92
ATOM 1484 CA TYR A 195 0 26.858 21.068 18.431 1.00 15.60
ATOM 1485 C TYR A 195 0 26.143 21.838 19.530 1.00 14.20
ATOM 1486 O TYR A 195 0 25.394 21.232 20.295 1.00 13.75
ATOM 1487 CB TYR A 195 0 25.814 20.880 17.300 1.00 16.13
15 ATOM 1488 CG TYR A 195 0 26.424 20.225 16.066 1.00 15.41
ATOM 1489 CD1 TYR A 195 0 26.663 18.851 16.091 1.00 15.91
ATOM 1490 CD2 TYR A 195 0 26.786 20.942 14.945 1.00 14.73
ATOM 1491 CE1 TYR A 195 0 27.244 18.204 15.010 1.00 16.55
ATOM 1492 CE2 TYR A 195 0 27.331 20.312 13.839 1.00 15.60
20 ATOM 1493 CZ TYR A 195 0 27.570 18.947 13.888 1.00 16.18
ATOM 1494 OH TYR A 195 0 28.144 18.287 12.831 1.00 15.64
ATOM 1495 N ARG A 196 0 26.366 23.136 19.561 1.00 12.74
ATOM 1496 CA ARG A 196 0 25.619 23.980 20.482 1.00 13.63
ATOM 1497 C ARG A 196 0 24.343 24.369 19.711 1.00 13.86
25 ATOM 1498 O ARG A 196 0 24.343 25.218 18.802 1.00 13.81
ATOM 1499 CB ARG A 196 0 26.379 25.187 20.991 1.00 13.96
ATOM 1500 CG ARG A 196 0 25.520 26.162 21.796 1.00 14.22
ATOM 1501 CD ARG A 196 0 26.337 27.238 22.438 1.00 15.27
ATOM 1502 NE ARG A 196 0 25.649 28.138 23.319 1.00 17.38
30 ATOM 1503 CZ ARG A 196 0 26.203 29.034 24.140 1.00 18.86
ATOM 1504 NH1 ARG A 196 0 27.540 29.141 24.217 1.00 16.30
ATOM 1505 NH2 ARG A 196 0 25.377 29.788 24.869 1.00 16.73
ATOM 1506 N MET A 197 0 23.266 23.624 20.002 1.00 13.86
ATOM 1507 CA MET A 197 0 21.980 23.932 19.340 1.00 12.98
35 ATOM 1508 C MET A 197 0 21.293 25.055 20.127 1.00 12.50
ATOM 1509 O MET A 197 0 21.285 24.997 21.359 1.00 13.93
ATOM 1510 CB MET A 197 0 21.118 22.693 19.266 1.00 12.50
ATOM 1511 CG MET A 197 0 21.762 21.567 18.447 1.00 13.94

	ATOM	1512	SD	MET A 197	0	21.860	22.033	16.735	1.00	16.62
	ATOM	1513	CE	MET A 197	0	22.157	20.467	15.927	1.00	16.37
	ATOM	1514	N	ARG A 198	0	20.768	26.064	19.450	1.00	11.00
	ATOM	1515	CA	ARG A 198	0	20.131	27.191	20.137	1.00	11.83
5	ATOM	1516	C	ARG A 198	0	18.624	27.130	19.868	1.00	12.36
	ATOM	1517	O	ARG A 198	0	18.145	27.304	18.731	1.00	10.03
	ATOM	1518	CB	ARG A 198	0	20.804	28.460	19.629	1.00	13.98
	ATOM	1519	CG	ARG A 198	0	22.282	28.567	20.065	1.00	16.25
	ATOM	1520	CD	ARG A 198	0	22.932	29.863	19.626	1.00	16.68
10	ATOM	1521	NE	ARG A 198	0	24.350	29.957	20.042	1.00	16.91
	ATOM	1522	CZ	ARG A 198	0	24.812	30.691	21.055	1.00	15.76
	ATOM	1523	NH1	ARG A 198	0	24.031	31.456	21.820	1.00	13.44
	ATOM	1524	NH2	ARG A 198	0	26.123	30.721	21.316	1.00	15.41
	ATOM	1525	N	LEU A 199	0	17.871	26.807	20.908	1.00	10.44
15	ATOM	1526	CA	LEU A 199	0	16.426	26.568	20.708	1.00	10.69
	ATOM	1527	C	LEU A 199	0	15.598	27.772	21.169	1.00	10.07
	ATOM	1528	O	LEU A 199	0	15.682	28.216	22.317	1.00	10.07
	ATOM	1529	CB	LEU A 199	0	16.003	25.317	21.491	1.00	8.67
	ATOM	1530	CG	LEU A 199	0	14.499	24.942	21.391	1.00	10.33
20	ATOM	1531	CD1	LEU A 199	0	14.193	24.333	20.023	1.00	8.13
	ATOM	1532	CD2	LEU A 199	0	14.170	23.907	22.485	1.00	9.10
	ATOM	1533	N	ILE A 200	0	14.857	28.370	20.242	1.00	10.46
	ATOM	1534	CA	ILE A 200	0	14.104	29.572	20.585	1.00	11.72
	ATOM	1535	C	ILE A 200	0	12.627	29.428	20.310	1.00	13.84
25	ATOM	1536	O	ILE A 200	0	12.254	29.059	19.192	1.00	13.22
	ATOM	1537	CB	ILE A 200	0	14.628	30.755	19.735	1.00	12.89
	ATOM	1538	CG1	ILE A 200	0	16.165	30.899	19.824	1.00	12.38
	ATOM	1539	CG2	ILE A 200	0	13.998	32.091	20.065	1.00	13.13
	ATOM	1540	CD1	ILE A 200	0	16.811	31.634	18.671	1.00	12.54
30	ATOM	1541	N	SER A 201	0	11.829	29.825	21.312	1.00	14.64
	ATOM	1542	CA	SER A 201	0	10.379	29.849	21.023	1.00	13.89
	ATOM	1543	C	SER A 201	0	10.018	31.280	20.608	1.00	11.10
	ATOM	1544	O	SER A 201	0	10.250	32.261	21.320	1.00	8.85
	ATOM	1545	CB	SER A 201	0	9.539	29.367	22.202	1.00	13.01
35	ATOM	1546	OG	SER A 201	0	8.313	30.047	22.207	1.00	12.19
	ATOM	1547	N	LEU A 202	0	9.428	31.376	19.438	1.00	9.64
	ATOM	1548	CA	LEU A 202	0	8.959	32.637	18.881	1.00	9.06
	ATOM	1549	C	LEU A 202	0	7.415	32.740	19.046	1.00	10.40

	ATOM	1550	O	LEU A 202	0	6.802	33.528	18.351	1.00	9.36
	ATOM	1551	CB	LEU A 202	0	9.239	32.618	17.379	1.00	9.09
	ATOM	1552	CG	LEU A 202	0	10.691	32.451	16.888	1.00	10.90
	ATOM	1553	CD1	LEU A 202	0	10.637	32.470	15.367	1.00	10.05
5	ATOM	1554	CD2	LEU A 202	0	11.617	33.559	17.414	1.00	8.56
	ATOM	1555	N	SER A 203	0	6.821	31.942	19.892	1.00	9.59
	ATOM	1556	CA	SER A 203	0	5.414	31.756	20.017	1.00	15.31
	ATOM	1557	C	SER A 203	0	4.624	32.960	20.544	1.00	16.67
	ATOM	1558	O	SER A 203	0	4.964	33.676	21.483	1.00	16.42
10	ATOM	1559	CB	SER A 203	0	5.130	30.505	20.867	1.00	15.21
	ATOM	1560	OG	SER A 203	0	3.742	30.240	21.004	1.00	17.14
	ATOM	1561	N	CYS A 204	0	3.428	33.051	19.984	1.00	17.18
	ATOM	1562	CA	CYS A 204	0	2.442	34.018	20.470	1.00	18.43
	ATOM	1563	C	CYS A 204	0	1.599	33.316	21.522	1.00	17.02
15	ATOM	1564	O	CYS A 204	0	0.867	34.039	22.200	1.00	17.27
	ATOM	1565	CB	CYS A 204	0	1.524	34.508	19.334	1.00	18.60
	ATOM	1566	SG	CYS A 204	0	2.135	36.038	18.612	1.00	20.23
	ATOM	1567	N	ASP A 205	0	1.687	31.989	21.665	1.00	16.38
	ATOM	1568	CA	ASP A 205	0	0.776	31.392	22.683	1.00	12.26
20	ATOM	1569	C	ASP A 205	0	1.123	30.002	23.087	1.00	11.34
	ATOM	1570	O	ASP A 205	0	1.432	29.687	24.255	1.00	11.40
	ATOM	1571	CB	ASP A 205	0	-0.622	31.516	22.076	1.00	14.87
	ATOM	1572	CG	ASP A 205	0	-1.729	30.881	22.892	1.00	16.61
	ATOM	1573	OD1	ASP A 205	0	-2.884	30.999	22.433	1.00	18.48
25	ATOM	1574	OD2	ASP A 205	0	-1.534	30.263	23.966	1.00	17.48
	ATOM	1575	N	PRO A 206	0	1.036	29.030	22.205	1.00	11.79
	ATOM	1576	CA	PRO A 206	0	1.313	27.639	22.542	1.00	11.91
	ATOM	1577	C	PRO A 206	0	2.739	27.411	23.045	1.00	14.01
	ATOM	1578	O	PRO A 206	0	3.676	28.135	22.661	1.00	14.38
30	ATOM	1579	CB	PRO A 206	0	1.124	26.816	21.262	1.00	11.87
	ATOM	1580	CG	PRO A 206	0	1.112	27.893	20.191	1.00	12.83
	ATOM	1581	CD	PRO A 206	0	0.749	29.241	20.766	1.00	11.09
	ATOM	1582	N	ASN A 207	0	2.888	26.439	23.911	1.00	13.06
	ATOM	1583	CA	ASN A 207	0	4.128	25.919	24.429	1.00	15.01
35	ATOM	1584	C	ASN A 207	0	4.332	24.591	23.677	1.00	15.84
	ATOM	1585	O	ASN A 207	0	3.376	24.095	23.038	1.00	16.22
	ATOM	1586	CB	ASN A 207	0	4.144	25.682	25.933	1.00	15.12
	ATOM	1587	CG	ASN A 207	0	3.054	24.708	26.395	1.00	19.36

	ATOM	1588	OD1	ASN	A 207	0	2.062	25.161	27.014	1.00	19.36
	ATOM	1589	ND2	ASN	A 207	0	3.174	23.408	26.203	1.00	16.49
	ATOM	1590	N	TRP	A 208	0	5.557	24.077	23.634	1.00	14.46
	ATOM	1591	CA	TRP	A 208	0	5.827	22.865	22.892	1.00	12.04
5	ATOM	1592	C	TRP	A 208	0	6.638	21.921	23.783	1.00	13.85
	ATOM	1593	O	TRP	A 208	0	7.482	22.385	24.558	1.00	13.02
	ATOM	1594	CB	TRP	A 208	0	6.654	23.136	21.628	1.00	11.91
	ATOM	1595	CG	TRP	A 208	0	5.951	23.769	20.465	1.00	11.27
	ATOM	1596	CD1	TRP	A 208	0	5.149	23.164	19.561	1.00	10.33
10	ATOM	1597	CD2	TRP	A 208	0	5.988	25.158	20.092	1.00	10.29
	ATOM	1598	NE1	TRP	A 208	0	4.698	24.078	18.625	1.00	10.91
	ATOM	1599	CE2	TRP	A 208	0	5.201	25.313	18.954	1.00	9.64
	ATOM	1600	CE3	TRP	A 208	0	6.634	26.294	20.625	1.00	10.25
	ATOM	1601	CZ2	TRP	A 208	0	5.011	26.553	18.344	1.00	8.53
15	ATOM	1602	CZ3	TRP	A 208	0	6.494	27.514	20.019	1.00	10.02
	ATOM	1603	CH2	TRP	A 208	0	5.668	27.633	18.881	1.00	11.79
	ATOM	1604	N	GLN	A 209	0	6.420	20.620	23.580	1.00	13.82
	ATOM	1605	CA	GLN	A 209	0	7.240	19.588	24.192	1.00	13.83
	ATOM	1606	C	GLN	A 209	0	8.251	19.281	23.075	1.00	13.07
20	ATOM	1607	O	GLN	A 209	0	7.848	18.968	21.948	1.00	14.18
	ATOM	1608	CB	GLN	A 209	0	6.441	18.319	24.487	1.00	15.65
	ATOM	1609	CG	GLN	A 209	0	5.449	18.481	25.649	1.00	17.26
	ATOM	1610	CD	GLN	A 209	0	6.177	18.514	26.975	1.00	18.17
	ATOM	1611	OE1	GLN	A 209	0	7.414	18.471	27.002	1.00	20.00
25	ATOM	1612	NE2	GLN	A 209	0	5.462	18.570	28.085	1.00	16.89
	ATOM	1613	N	PHE	A 210	0	9.538	19.461	23.351	1.00	11.26
	ATOM	1614	CA	PHE	A 210	0	10.526	19.329	22.287	1.00	10.01
	ATOM	1615	C	PHE	A 210	0	11.457	18.153	22.585	1.00	9.18
	ATOM	1616	O	PHE	A 210	0	11.894	17.999	23.732	1.00	10.07
30	ATOM	1617	CB	PHE	A 210	0	11.370	20.629	22.292	1.00	10.86
	ATOM	1618	CG	PHE	A 210	0	12.489	20.581	21.292	1.00	9.63
	ATOM	1619	CD1	PHE	A 210	0	13.760	20.179	21.674	1.00	9.95
	ATOM	1620	CD2	PHE	A 210	0	12.251	20.922	19.984	1.00	8.54
	ATOM	1621	CE1	PHE	A 210	0	14.778	20.150	20.738	1.00	9.23
35	ATOM	1622	CE2	PHE	A 210	0	13.243	20.862	19.023	1.00	7.93
	ATOM	1623	CZ	PHE	A 210	0	14.520	20.491	19.426	1.00	8.71
	ATOM	1624	N	SER	A 211	0	11.741	17.384	21.545	1.00	8.62
	ATOM	1625	CA	SER	A 211	0	12.645	16.255	21.716	1.00	10.71

ATOM 1626 C SER A 211 O 13.142 15.844 20.347 1.00 11.36
ATOM 1627 O SER A 211 O 12.661 16.323 19.315 1.00 9.99
ATOM 1628 CB SER A 211 O 11.970 15.070 22.427 1.00 10.56
ATOM 1629 OG SER A 211 O 10.899 14.731 21.513 1.00 12.92
5 ATOM 1630 N ILE A 212 O 14.268 15.122 20.390 1.00 13.67
ATOM 1631 CA ILE A 212 O 14.883 14.680 19.131 1.00 14.79
ATOM 1632 C ILE A 212 O 15.013 13.166 19.220 1.00 15.44
ATOM 1633 O ILE A 212 O 15.624 12.689 20.177 1.00 15.98
ATOM 1634 CB ILE A 212 O 16.255 15.341 18.887 1.00 17.04
10 ATOM 1635 CG1 ILE A 212 O 16.082 16.859 18.756 1.00 15.64
ATOM 1636 CG2 ILE A 212 O 16.935 14.722 17.648 1.00 15.24
ATOM 1637 CD1 ILE A 212 O 17.352 17.648 18.553 1.00 16.57
ATOM 1638 N ASP A 213 O 14.453 12.418 18.281 1.00 15.53
ATOM 1639 CA ASP A 213 O 14.549 10.952 18.401 1.00 16.50
15 ATOM 1640 C ASP A 213 O 16.004 10.469 18.541 1.00 16.69
ATOM 1641 O ASP A 213 O 16.948 10.902 17.851 1.00 14.36
ATOM 1642 CB ASP A 213 O 13.884 10.359 17.173 1.00 17.15
ATOM 1643 CG ASP A 213 O 12.369 10.467 17.144 1.00 18.12
ATOM 1644 OD1 ASP A 213 O 11.751 10.995 18.092 1.00 16.90
20 ATOM 1645 OD2 ASP A 213 O 11.801 9.990 16.129 1.00 17.35
ATOM 1646 N GLY A 214 O 16.198 9.559 19.477 1.00 15.76
ATOM 1647 CA GLY A 214 O 17.457 8.900 19.747 1.00 17.22
ATOM 1648 C GLY A 214 O 18.548 9.757 20.368 1.00 18.54
ATOM 1649 O GLY A 214 O 19.680 9.277 20.404 1.00 18.20
25 ATOM 1650 N HIS A 215 O 18.341 11.024 20.738 1.00 18.17
ATOM 1651 CA HIS A 215 O 19.422 11.880 21.229 1.00 17.59
ATOM 1652 C HIS A 215 O 19.096 12.505 22.577 1.00 17.92
ATOM 1653 O HIS A 215 O 17.917 12.696 22.898 1.00 20.45
ATOM 1654 CB HIS A 215 O 19.705 13.008 20.221 1.00 15.73
30 ATOM 1655 CG HIS A 215 O 20.309 12.543 18.936 1.00 16.90
ATOM 1656 ND1 HIS A 215 O 19.589 11.864 17.963 1.00 17.35
ATOM 1657 CD2 HIS A 215 O 21.574 12.658 18.444 1.00 16.15
ATOM 1658 CE1 HIS A 215 O 20.376 11.576 16.933 1.00 17.63
ATOM 1659 NE2 HIS A 215 O 21.599 12.046 17.216 1.00 17.73
35 ATOM 1660 N GLU A 216 O 20.104 12.815 23.382 1.00 17.22
ATOM 1661 CA GLU A 216 O 19.876 13.479 24.665 1.00 15.86
ATOM 1662 C GLU A 216 O 20.070 14.976 24.456 1.00 15.61
ATOM 1663 O GLU A 216 O 20.684 15.386 23.453 1.00 14.96

ATOM 1664 CB GLU A 216 0 20.817 12.901 25.694 1.00 15.38
ATOM 1665 CG GLU A 216 0 20.440 11.520 26.166 1.00 16.53
ATOM 1666 CD GLU A 216 0 21.242 11.058 27.357 1.00 17.23
ATOM 1667 OE1 GLU A 216 0 22.378 10.619 27.129 1.00 20.31
5 ATOM 1668 OE2 GLU A 216 0 20.813 11.119 28.519 1.00 16.06
ATOM 1669 N LEU A 217 0 19.623 15.792 25.394 1.00 14.64
ATOM 1670 CA LEU A 217 0 19.738 17.243 25.251 1.00 14.91
ATOM 1671 C LEU A 217 0 20.512 17.792 26.446 1.00 14.71
ATOM 1672 O LEU A 217 0 19.950 17.734 27.539 1.00 15.67
10 ATOM 1673 CB LEU A 217 0 18.362 17.931 25.229 1.00 14.75
ATOM 1674 CG LEU A 217 0 17.276 17.349 24.306 1.00 15.40
ATOM 1675 CD1 LEU A 217 0 15.939 18.075 24.505 1.00 15.08
ATOM 1676 CD2 LEU A 217 0 17.723 17.453 22.849 1.00 15.22
ATOM 1677 N THR A 218 0 21.732 18.278 26.229 1.00 13.65
15 ATOM 1678 CA THR A 218 0 22.507 18.714 27.402 1.00 13.26
ATOM 1679 C THR A 218 0 22.427 20.232 27.505 1.00 13.27
ATOM 1680 O THR A 218 0 23.142 20.955 26.805 1.00 12.91
ATOM 1681 CB THR A 218 0 23.955 18.216 27.304 1.00 12.08
ATOM 1682 OG1 THR A 218 0 23.935 16.782 27.331 1.00 15.48
20 ATOM 1683 CG2 THR A 218 0 24.767 18.721 28.470 1.00 11.46
ATOM 1684 N ILE A 219 0 21.522 20.649 28.385 1.00 13.30
ATOM 1685 CA ILE A 219 0 21.259 22.068 28.547 1.00 14.53
ATOM 1686 C ILE A 219 0 22.420 22.818 29.180 1.00 12.72
ATOM 1687 O ILE A 219 0 22.795 22.492 30.292 1.00 13.08
25 ATOM 1688 CB ILE A 219 0 19.930 22.268 29.323 1.00 14.74
ATOM 1689 CG1 ILE A 219 0 18.761 21.699 28.441 1.00 17.33
ATOM 1690 CG2 ILE A 219 0 19.666 23.717 29.656 1.00 13.40
ATOM 1691 CD1 ILE A 219 0 17.597 21.481 29.412 1.00 19.42
ATOM 1692 N ILE A 220 0 22.898 23.869 28.510 1.00 12.55
30 ATOM 1693 CA ILE A 220 0 23.994 24.696 29.019 1.00 13.25
ATOM 1694 C ILE A 220 0 23.686 26.193 29.085 1.00 15.11
ATOM 1695 O ILE A 220 0 24.477 27.001 29.618 1.00 14.73
ATOM 1696 CB ILE A 220 0 25.239 24.507 28.125 1.00 11.80
ATOM 1697 CG1 ILE A 220 0 24.954 24.871 26.671 1.00 10.93
35 ATOM 1698 CG2 ILE A 220 0 25.770 23.072 28.291 1.00 9.59
ATOM 1699 CD1 ILE A 220 0 26.249 25.231 25.928 1.00 12.07
ATOM 1700 N GLU A 221 0 22.490 26.573 28.597 1.00 13.30
ATOM 1701 CA GLU A 221 0 22.048 27.951 28.624 1.00 12.96

	ATOM	1702	C	GLU A 221	0	20.522	28.066	28.727	1.00	13.77
	ATOM	1703	O	GLU A 221	0	19.799	27.301	28.068	1.00	14.06
	ATOM	1704	CB	GLU A 221	0	22.436	28.666	27.318	1.00	12.73
	ATOM	1705	CG	GLU A 221	0	22.280	30.178	27.325	1.00	12.94
5	ATOM	1706	CD	GLU A 221	0	22.018	30.783	25.969	1.00	13.84
	ATOM	1707	OE1	GLU A 221	0	22.345	30.269	24.887	1.00	12.66
	ATOM	1708	OE2	GLU A 221	0	21.386	31.862	25.936	1.00	14.80
	ATOM	1709	N	VAL A 222	0	20.062	29.091	29.434	1.00	13.89
	ATOM	1710	CA	VAL A 222	0	18.632	29.350	29.534	1.00	14.13
10	ATOM	1711	C	VAL A 222	0	18.409	30.853	29.493	1.00	13.87
	ATOM	1712	O	VAL A 222	0	18.900	31.657	30.300	1.00	11.55
	ATOM	1713	CB	VAL A 222	0	18.003	28.649	30.737	1.00	16.86
	ATOM	1714	CG1	VAL A 222	0	18.730	28.941	32.017	1.00	19.16
	ATOM	1715	CG2	VAL A 222	0	16.575	29.120	31.033	1.00	18.45
15	ATOM	1716	N	ASP A 223	0	17.631	31.267	28.481	1.00	11.69
	ATOM	1717	CA	ASP A 223	0	17.245	32.673	28.386	1.00	13.60
	ATOM	1718	C	ASP A 223	0	18.472	33.598	28.548	1.00	14.44
	ATOM	1719	O	ASP A 223	0	18.423	34.552	29.336	1.00	12.75
	ATOM	1720	CB	ASP A 223	0	16.161	33.033	29.417	1.00	12.59
20	ATOM	1721	CG	ASP A 223	0	14.845	32.279	29.364	1.00	14.64
	ATOM	1722	OD1	ASP A 223	0	14.697	31.397	28.493	1.00	13.34
	ATOM	1723	OD2	ASP A 223	0	13.858	32.463	30.156	1.00	13.85
	ATOM	1724	N	GLY A 224	0	19.544	33.372	27.767	1.00	13.49
	ATOM	1725	CA	GLY A 224	0	20.728	34.213	27.770	1.00	12.85
25	ATOM	1726	C	GLY A 224	0	21.562	34.112	29.049	1.00	13.00
	ATOM	1727	O	GLY A 224	0	22.326	35.040	29.317	1.00	13.97
	ATOM	1728	N	GLU A 225	0	21.370	33.105	29.875	1.00	11.78
	ATOM	1729	CA	GLU A 225	0	22.068	32.888	31.114	1.00	14.97
	ATOM	1730	C	GLU A 225	0	22.609	31.447	31.106	1.00	16.73
30	ATOM	1731	O	GLU A 225	0	21.858	30.498	30.849	1.00	15.88
	ATOM	1732	CB	GLU A 225	0	21.174	33.062	32.358	1.00	16.54
	ATOM	1733	CG	GLU A 225	0	20.509	34.424	32.534	1.00	16.30
	ATOM	1734	CD	GLU A 225	0	21.492	35.546	32.823	1.00	17.57
	ATOM	1735	OE1	GLU A 225	0	22.450	35.254	33.561	1.00	18.76
35	ATOM	1736	OE2	GLU A 225	0	21.360	36.711	32.360	1.00	17.77
	ATOM	1737	N	LEU A 226	0	23.922	31.285	31.324	1.00	16.90
	ATOM	1738	CA	LEU A 226	0	24.526	29.955	31.318	1.00	15.50
	ATOM	1739	C	LEU A 226	0	24.183	29.127	32.540	1.00	15.04

ATOM 1740 O LEU A 226 O 24.002 29.648 33.652 1.00 15.17
ATOM 1741 CB LEU A 226 O 26.062 30.008 31.216 1.00 15.36
ATOM 1742 CG LEU A 226 O 26.567 30.741 29.958 1.00 17.95
ATOM 1743 CD1 LEU A 226 O 28.076 30.876 29.979 1.00 18.77
5 ATOM 1744 CD2 LEU A 226 O 26.111 30.029 28.687 1.00 17.36
ATOM 1745 N THR A 227 O 24.119 27.799 32.332 1.00 13.62
ATOM 1746 CA THR A 227 O 23.848 26.930 33.479 1.00 13.72
ATOM 1747 C THR A 227 O 24.936 25.851 33.528 1.00 14.30
ATOM 1748 O THR A 227 O 25.732 25.629 32.592 1.00 14.28
10 ATOM 1749 CB THR A 227 O 22.478 26.217 33.352 1.00 14.35
ATOM 1750 OG1 THR A 227 O 22.506 25.385 32.178 1.00 13.68
ATOM 1751 CG2 THR A 227 O 21.284 27.161 33.180 1.00 12.29
ATOM 1752 N GLU A 228 O 24.960 25.136 34.625 1.00 14.73
ATOM 1753 CA GLU A 228 O 25.765 23.907 34.714 1.00 17.32
15 ATOM 1754 C GLU A 228 O 25.110 22.971 33.680 1.00 17.30
ATOM 1755 O GLU A 228 O 23.917 23.035 33.472 1.00 16.97
ATOM 1756 CB GLU A 228 O 25.617 23.315 36.114 1.00 16.58
ATOM 1757 CG GLU A 228 O 26.493 23.979 37.186 1.00 18.10
ATOM 1758 CD GLU A 228 O 26.236 23.458 38.575 1.00 20.92
20 ATOM 1759 OE1 GLU A 228 O 25.469 22.470 38.755 1.00 23.38
ATOM 1760 OE2 GLU A 228 O 26.769 23.997 39.564 1.00 21.26
ATOM 1761 N PRO A 229 O 25.867 22.158 32.984 1.00 16.91
ATOM 1762 CA PRO A 229 O 25.369 21.207 31.992 1.00 16.37
ATOM 1763 C PRO A 229 O 24.351 20.275 32.599 1.00 16.24
25 ATOM 1764 O PRO A 229 O 24.624 19.652 33.619 1.00 15.76
ATOM 1765 CB PRO A 229 O 26.612 20.469 31.419 1.00 15.97
ATOM 1766 CG PRO A 229 O 27.701 21.509 31.741 1.00 15.92
ATOM 1767 CD PRO A 229 O 27.337 22.141 33.083 1.00 14.86
ATOM 1768 N HIS A 230 O 23.140 20.164 32.038 1.00 15.58
30 ATOM 1769 CA HIS A 230 O 22.090 19.325 32.618 1.00 15.01
ATOM 1770 C HIS A 230 O 21.354 18.610 31.488 1.00 13.55
ATOM 1771 O HIS A 230 O 20.756 19.192 30.590 1.00 13.47
ATOM 1772 CB HIS A 230 O 21.172 20.164 33.510 1.00 15.89
ATOM 1773 CG HIS A 230 O 20.045 19.341 34.064 1.00 18.32
35 ATOM 1774 ND1 HIS A 230 O 20.252 18.347 35.004 1.00 18.14
ATOM 1775 CD2 HIS A 230 O 18.713 19.328 33.791 1.00 17.75
ATOM 1776 CE1 HIS A 230 O 19.121 17.768 35.310 1.00 16.33
ATOM 1777 NE2 HIS A 230 O 18.173 18.344 34.609 1.00 17.85

ATOM 1778 N THR A 231 O 21.496 17.304 31.458 1.00 12.94
ATOM 1779 CA THR A 231 O 20.995 16.474 30.346 1.00 14.15
ATOM 1780 C THR A 231 O 19.620 15.890 30.547 1.00 13.41
ATOM 1781 O THR A 231 O 19.293 15.401 31.616 1.00 14.89
5 ATOM 1782 CB THR A 231 O 22.040 15.364 30.060 1.00 13.73
ATOM 1783 OG1 THR A 231 O 23.314 16.023 29.852 1.00 14.77
ATOM 1784 CG2 THR A 231 O 21.655 14.600 28.818 1.00 13.06
ATOM 1785 N VAL A 232 O 18.776 15.954 29.549 1.00 12.86
ATOM 1786 CA VAL A 232 O 17.374 15.505 29.665 1.00 13.44
10 ATOM 1787 C VAL A 232 O 16.999 14.966 28.319 1.00 14.96
ATOM 1788 O VAL A 232 O 17.790 15.258 27.390 1.00 14.12
ATOM 1789 CB VAL A 232 O 16.771 16.910 30.000 1.00 17.41
ATOM 1790 CG1 VAL A 232 O 16.075 17.587 28.856 1.00 14.66
ATOM 1791 CG2 VAL A 232 O 16.158 16.935 31.371 1.00 15.66
15 ATOM 1792 N ASP A 233 O 15.874 14.277 28.153 1.00 14.01
ATOM 1793 CA ASP A 233 O 15.405 13.803 26.874 1.00 14.73
ATOM 1794 C ASP A 233 O 14.353 14.718 26.245 1.00 14.74
ATOM 1795 O ASP A 233 O 14.187 14.731 25.027 1.00 13.41
ATOM 1796 CB ASP A 233 O 14.640 12.465 27.046 1.00 16.54
20 ATOM 1797 CG ASP A 233 O 15.637 11.417 27.536 1.00 19.27
ATOM 1798 OD1 ASP A 233 O 16.543 11.145 26.732 1.00 20.98
ATOM 1799 OD2 ASP A 233 O 15.536 10.945 28.667 1.00 19.27
ATOM 1800 N ARG A 234 O 13.595 15.386 27.122 1.00 13.79
ATOM 1801 CA ARG A 234 O 12.514 16.199 26.598 1.00 16.36
25 ATOM 1802 C ARG A 234 O 12.258 17.426 27.472 1.00 15.17
ATOM 1803 O ARG A 234 O 12.418 17.390 28.686 1.00 13.96
ATOM 1804 CB ARG A 234 O 11.265 15.330 26.482 1.00 19.23
ATOM 1805 CG ARG A 234 O 10.104 16.036 25.788 1.00 22.25
ATOM 1806 CD ARG A 234 O 8.981 15.023 25.506 1.00 24.68
30 ATOM 1807 NE ARG A 234 O 8.157 14.983 26.705 1.00 28.27
ATOM 1808 CZ ARG A 234 O 6.845 14.828 26.719 1.00 28.66
ATOM 1809 NH1 ARG A 234 O 6.291 14.833 27.909 1.00 30.08
ATOM 1810 NH2 ARG A 234 O 6.191 14.662 25.587 1.00 30.24
ATOM 1811 N LEU A 235 O 11.874 18.524 26.816 1.00 13.90
35 ATOM 1812 CA LEU A 235 O 11.619 19.742 27.607 1.00 13.15
ATOM 1813 C LEU A 235 O 10.390 20.430 27.041 1.00 11.49
ATOM 1814 O LEU A 235 O 10.025 20.304 25.873 1.00 11.08
ATOM 1815 CB LEU A 235 O 12.825 20.630 27.695 1.00 14.39

	ATOM	1816	CG	LEU A 235	0	13.459	21.645	26.801	1.00	17.19
	ATOM	1817	CD1	LEU A 235	0	14.795	21.218	26.197	1.00	16.98
	ATOM	1818	CD2	LEU A 235	0	12.586	22.219	25.685	1.00	18.24
	ATOM	1819	N	GLN A 236	0	9.769	21.152	27.949	1.00	12.74
5	ATOM	1820	CA	GLN A 236	0	8.576	21.944	27.616	1.00	13.45
	ATOM	1821	C	GLN A 236	0	9.005	23.390	27.459	1.00	12.21
	ATOM	1822	O	GLN A 236	0	9.606	23.939	28.406	1.00	13.90
	ATOM	1823	CB	GLN A 236	0	7.525	21.770	28.741	1.00	12.06
	ATOM	1824	CG	GLN A 236	0	6.197	22.276	28.238	1.00	14.12
10	ATOM	1825	CD	GLN A 236	0	5.025	22.108	29.205	1.00	13.35
	ATOM	1826	OE1	GLN A 236	0	3.893	22.215	28.721	1.00	15.61
	ATOM	1827	NE2	GLN A 236	0	5.226	21.912	30.463	1.00	12.00
	ATOM	1828	N	ILE A 237	0	8.748	24.011	26.311	1.00	12.17
	ATOM	1829	CA	ILE A 237	0	9.213	25.390	26.156	1.00	12.41
15	ATOM	1830	C	ILE A 237	0	8.061	26.376	25.953	1.00	13.14
	ATOM	1831	O	ILE A 237	0	7.283	26.310	24.990	1.00	13.64
	ATOM	1832	CB	ILE A 237	0	10.255	25.437	25.022	1.00	11.03
	ATOM	1833	CG1	ILE A 237	0	10.947	26.793	24.960	1.00	11.84
	ATOM	1834	CG2	ILE A 237	0	9.615	25.086	23.662	1.00	10.02
20	ATOM	1835	CD1	ILE A 237	0	12.041	26.953	23.902	1.00	11.23
	ATOM	1836	N	PHE A 238	0	8.037	27.414	26.765	1.00	12.83
	ATOM	1837	CA	PHE A 238	0	6.979	28.431	26.714	1.00	13.23
	ATOM	1838	C	PHE A 238	0	7.382	29.683	25.957	1.00	13.99
	ATOM	1839	O	PHE A 238	0	8.530	29.848	25.545	1.00	13.87
25	ATOM	1840	CB	PHE A 238	0	6.592	28.848	28.145	1.00	12.72
	ATOM	1841	CG	PHE A 238	0	6.176	27.691	28.993	1.00	14.51
	ATOM	1842	CD1	PHE A 238	0	7.098	26.957	29.710	1.00	14.84
	ATOM	1843	CD2	PHE A 238	0	4.836	27.314	29.078	1.00	15.50
	ATOM	1844	CE1	PHE A 238	0	6.748	25.882	30.497	1.00	13.87
30	ATOM	1845	CE2	PHE A 238	0	4.468	26.236	29.862	1.00	14.62
	ATOM	1846	CZ	PHE A 238	0	5.423	25.528	30.568	1.00	15.15
	ATOM	1847	N	THR A 239	0	6.388	30.494	25.604	1.00	14.16
	ATOM	1848	CA	THR A 239	0	6.543	31.678	24.806	1.00	13.44
	ATOM	1849	C	THR A 239	0	7.832	32.453	25.106	1.00	11.74
35	ATOM	1850	O	THR A 239	0	8.012	32.950	26.218	1.00	10.47
	ATOM	1851	CB	THR A 239	0	5.381	32.695	24.978	1.00	15.55
	ATOM	1852	OG1	THR A 239	0	5.258	33.008	26.359	1.00	17.88
	ATOM	1853	CG2	THR A 239	0	4.055	32.131	24.478	1.00	16.75

	ATOM	1854	N	GLY A 240	0	8.672	32.593	24.078	1.00	7.94
	ATOM	1855	CA	GLY A 240	0	9.877	33.348	24.193	1.00	10.08
	ATOM	1856	C	GLY A 240	0	11.039	32.865	25.041	1.00	11.34
	ATOM	1857	O	GLY A 240	0	11.977	33.650	25.216	1.00	11.02
5	ATOM	1858	N	GLN A 241	0	10.990	31.646	25.592	1.00	9.73
	ATOM	1859	CA	GLN A 241	0	12.067	31.090	26.364	1.00	9.59
	ATOM	1860	C	GLN A 241	0	13.114	30.587	25.342	1.00	10.56
	ATOM	1861	O	GLN A 241	0	12.823	30.467	24.126	1.00	8.44
	ATOM	1862	CB	GLN A 241	0	11.604	29.965	27.285	1.00	10.57
10	ATOM	1863	CG	GLN A 241	0	10.820	30.363	28.523	1.00	10.54
	ATOM	1864	CD	GLN A 241	0	10.341	29.190	29.341	1.00	12.22
	ATOM	1865	OE1	GLN A 241	0	10.118	28.077	28.815	1.00	13.21
	ATOM	1866	NE2	GLN A 241	0	10.220	29.466	30.639	1.00	11.74
	ATOM	1867	N	ARG A 242	0	14.372	30.492	25.774	1.00	9.00
15	ATOM	1868	CA	ARG A 242	0	15.388	29.992	24.834	1.00	11.01
	ATOM	1869	C	ARG A 242	0	16.210	28.966	25.609	1.00	11.30
	ATOM	1870	O	ARG A 242	0	16.292	29.133	26.816	1.00	9.51
	ATOM	1871	CB	ARG A 242	0	16.324	31.043	24.265	1.00	12.77
	ATOM	1872	CG	ARG A 242	0	15.694	32.128	23.364	1.00	12.52
20	ATOM	1873	CD	ARG A 242	0	15.066	33.249	24.138	1.00	10.81
	ATOM	1874	NE	ARG A 242	0	15.957	34.126	24.892	1.00	10.80
	ATOM	1875	CZ	ARG A 242	0	15.630	34.761	26.002	1.00	11.36
	ATOM	1876	NH1	ARG A 242	0	16.486	35.548	26.648	1.00	7.98
	ATOM	1877	NH2	ARG A 242	0	14.365	34.589	26.489	1.00	12.78
25	ATOM	1878	N	TYR A 243	0	16.717	27.934	24.942	1.00	11.61
	ATOM	1879	CA	TYR A 243	0	17.631	27.009	25.610	1.00	12.54
	ATOM	1880	C	TYR A 243	0	18.819	26.762	24.650	1.00	14.46
	ATOM	1881	O	TYR A 243	0	18.568	26.656	23.435	1.00	16.11
	ATOM	1882	CB	TYR A 243	0	17.015	25.638	25.934	1.00	11.09
30	ATOM	1883	CG	TYR A 243	0	16.007	25.667	27.054	1.00	12.11
	ATOM	1884	CD1	TYR A 243	0	14.641	25.825	26.843	1.00	12.88
	ATOM	1885	CD2	TYR A 243	0	16.440	25.575	28.371	1.00	12.11
	ATOM	1886	CE1	TYR A 243	0	13.748	25.869	27.915	1.00	12.71
	ATOM	1887	CE2	TYR A 243	0	15.560	25.582	29.436	1.00	12.50
35	ATOM	1888	CZ	TYR A 243	0	14.205	25.738	29.188	1.00	12.29
	ATOM	1889	OH	TYR A 243	0	13.379	25.789	30.286	1.00	13.65
	ATOM	1890	N	SER A 244	0	20.059	26.734	25.144	1.00	12.78
	ATOM	1891	CA	SER A 244	0	21.117	26.212	24.268	1.00	13.22

	ATOM	1892	C	SER A 244	0	21.333	24.779	24.814	1.00	11.06
	ATOM	1893	O	SER A 244	0	21.377	24.604	26.018	1.00	11.27
	ATOM	1894	CB	SER A 244	0	22.485	26.907	24.308	1.00	14.46
	ATOM	1895	OG	SER A 244	0	22.551	28.029	23.463	1.00	13.59
5	ATOM	1896	N	PHE A 245	0	21.484	23.780	23.983	1.00	11.89
	ATOM	1897	CA	PHE A 245	0	21.772	22.437	24.452	1.00	13.14
	ATOM	1898	C	PHE A 245	0	22.867	21.857	23.546	1.00	12.32
	ATOM	1899	O	PHE A 245	0	22.890	22.128	22.354	1.00	11.11
	ATOM	1900	CB	PHE A 245	0	20.554	21.495	24.526	1.00	11.40
10	ATOM	1901	CG	PHE A 245	0	19.915	21.236	23.195	1.00	11.98
	ATOM	1902	CD1	PHE A 245	0	18.815	21.993	22.813	1.00	13.38
	ATOM	1903	CD2	PHE A 245	0	20.349	20.236	22.351	1.00	11.45
	ATOM	1904	CE1	PHE A 245	0	18.216	21.773	21.588	1.00	12.84
	ATOM	1905	CE2	PHE A 245	0	19.759	20.000	21.129	1.00	11.48
15	ATOM	1906	CZ	PHE A 245	0	18.705	20.796	20.743	1.00	12.65
	ATOM	1907	N	VAL A 246	0	23.742	21.073	24.169	1.00	13.51
	ATOM	1908	CA	VAL A 246	0	24.775	20.427	23.341	1.00	13.37
	ATOM	1909	C	VAL A 246	0	24.096	19.177	22.783	1.00	12.47
	ATOM	1910	O	VAL A 246	0	23.505	18.425	23.540	1.00	11.41
20	ATOM	1911	CB	VAL A 246	0	25.990	19.984	24.190	1.00	14.96
	ATOM	1912	CG1	VAL A 246	0	26.995	19.186	23.364	1.00	13.75
	ATOM	1913	CG2	VAL A 246	0	26.681	21.165	24.841	1.00	15.92
	ATOM	1914	N	LEU A 247	0	24.160	18.996	21.490	1.00	12.97
	ATOM	1915	CA	LEU A 247	0	23.766	17.833	20.785	1.00	14.32
25	ATOM	1916	C	LEU A 247	0	25.071	17.077	20.395	1.00	14.22
	ATOM	1917	O	LEU A 247	0	25.954	17.529	19.664	1.00	12.45
	ATOM	1918	CB	LEU A 247	0	22.980	18.109	19.505	1.00	16.00
	ATOM	1919	CG	LEU A 247	0	22.514	16.786	18.835	1.00	16.80
	ATOM	1920	CD1	LEU A 247	0	21.266	16.306	19.513	1.00	18.30
30	ATOM	1921	CD2	LEU A 247	0	22.207	16.988	17.373	1.00	18.70
	ATOM	1922	N	ASP A 248	0	25.144	15.886	20.926	1.00	13.56
	ATOM	1923	CA	ASP A 248	0	26.278	14.980	20.727	1.00	16.65
	ATOM	1924	C	ASP A 248	0	25.916	14.072	19.581	1.00	16.18
	ATOM	1925	O	ASP A 248	0	25.095	13.166	19.813	1.00	17.60
35	ATOM	1926	CB	ASP A 248	0	26.536	14.229	22.036	1.00	17.83
	ATOM	1927	CG	ASP A 248	0	27.798	13.359	22.024	1.00	21.77
	ATOM	1928	OD1	ASP A 248	0	28.231	12.967	23.140	1.00	24.11
	ATOM	1929	OD2	ASP A 248	0	28.345	13.060	20.950	1.00	21.25

	ATOM	1930	N	ALA A 249	0	26.414	14.277	18.369	1.00	15.85
	ATOM	1931	CA	ALA A 249	0	25.982	13.416	17.255	1.00	17.99
	ATOM	1932	C	ALA A 249	0	26.698	12.049	17.306	1.00	20.21
	ATOM	1933	O	ALA A 249	0	27.569	11.766	16.485	1.00	19.11
5	ATOM	1934	CB	ALA A 249	0	26.165	14.126	15.930	1.00	14.57
	ATOM	1935	N	ASN A 250	0	26.273	11.223	18.253	1.00	21.66
	ATOM	1936	CA	ASN A 250	0	26.861	9.961	18.581	1.00	25.53
	ATOM	1937	C	ASN A 250	0	26.061	8.721	18.202	1.00	27.30
	ATOM	1938	O	ASN A 250	0	26.344	7.645	18.756	1.00	29.42
10	ATOM	1939	CB	ASN A 250	0	27.108	9.912	20.104	1.00	25.83
	ATOM	1940	CG	ASN A 250	0	25.888	9.968	20.978	1.00	28.76
	ATOM	1941	OD1	ASN A 250	0	24.757	10.156	20.527	1.00	29.90
	ATOM	1942	ND2	ASN A 250	0	26.042	9.826	22.306	1.00	29.52
	ATOM	1943	N	GLN A 251	0	25.089	8.841	17.302	1.00	26.74
15	ATOM	1944	CA	GLN A 251	0	24.239	7.712	16.934	1.00	23.48
	ATOM	1945	C	GLN A 251	0	24.583	7.311	15.510	1.00	21.73
	ATOM	1946	O	GLN A 251	0	25.333	8.009	14.843	1.00	19.39
	ATOM	1947	CB	GLN A 251	0	22.757	8.104	17.022	1.00	24.79
	ATOM	1948	CG	GLN A 251	0	22.333	8.701	18.360	1.00	25.14
20	ATOM	1949	CD	GLN A 251	0	22.430	7.693	19.480	1.00	26.76
	ATOM	1950	OE1	GLN A 251	0	21.762	6.654	19.405	1.00	28.78
	ATOM	1951	NE2	GLN A 251	0	23.202	7.986	20.514	1.00	26.02
	ATOM	1952	N	PRO A 252	0	24.058	6.177	15.076	1.00	20.53
	ATOM	1953	CA	PRO A 252	0	24.293	5.637	13.755	1.00	20.06
25	ATOM	1954	C	PRO A 252	0	23.940	6.671	12.702	1.00	21.83
	ATOM	1955	O	PRO A 252	0	22.973	7.424	12.940	1.00	22.51
	ATOM	1956	CB	PRO A 252	0	23.417	4.367	13.647	1.00	19.98
	ATOM	1957	CG	PRO A 252	0	23.288	3.997	15.096	1.00	19.94
	ATOM	1958	CD	PRO A 252	0	23.223	5.289	15.902	1.00	19.68
30	ATOM	1959	N	VAL A 253	0	24.663	6.728	11.584	1.00	20.85
	ATOM	1960	CA	VAL A 253	0	24.302	7.741	10.604	1.00	22.29
	ATOM	1961	C	VAL A 253	0	22.897	7.414	10.108	1.00	23.02
	ATOM	1962	O	VAL A 253	0	22.593	6.289	9.753	1.00	21.37
	ATOM	1963	CB	VAL A 253	0	25.298	8.065	9.494	1.00	23.22
35	ATOM	1964	CG1	VAL A 253	0	26.696	7.582	9.827	1.00	22.25
	ATOM	1965	CG2	VAL A 253	0	24.859	7.680	8.101	1.00	22.26
	ATOM	1966	N	ASP A 254	0	22.012	8.422	10.159	1.00	24.32
	ATOM	1967	CA	ASP A 254	0	20.613	8.176	9.786	1.00	22.09

	ATOM	1968	C	ASP A 254	0	19.782	9.448	9.821	1.00	20.71
	ATOM	1969	O	ASP A 254	0	20.365	10.481	10.099	1.00	18.92
	ATOM	1970	CB	ASP A 254	0	20.048	7.211	10.830	1.00	23.39
	ATOM	1971	CG	ASP A 254	0	18.964	6.331	10.251	1.00	24.43
5	ATOM	1972	OD1	ASP A 254	0	18.355	6.663	9.239	1.00	23.21
	ATOM	1973	OD2	ASP A 254	0	18.736	5.244	10.816	1.00	28.26
	ATOM	1974	N	ASN A 255	0	18.485	9.338	9.496	1.00	18.97
	ATOM	1975	CA	ASN A 255	0	17.583	10.479	9.599	1.00	17.69
	ATOM	1976	C	ASN A 255	0	16.785	10.335	10.889	1.00	17.64
10	ATOM	1977	O	ASN A 255	0	16.390	9.204	11.249	1.00	17.75
	ATOM	1978	CB	ASN A 255	0	16.663	10.554	8.386	1.00	17.19
	ATOM	1979	CG	ASN A 255	0	17.467	10.882	7.143	1.00	17.33
	ATOM	1980	OD1	ASN A 255	0	17.891	12.023	6.932	1.00	18.05
	ATOM	1981	ND2	ASN A 255	0	17.649	9.913	6.263	1.00	15.98
15	ATOM	1982	N	TYR A 256	0	16.657	11.403	11.684	1.00	14.89
	ATOM	1983	CA	TYR A 256	0	15.983	11.364	12.961	1.00	12.56
	ATOM	1984	C	TYR A 256	0	14.966	12.520	12.991	1.00	15.02
	ATOM	1985	O	TYR A 256	0	15.208	13.637	12.509	1.00	14.49
	ATOM	1986	CB	TYR A 256	0	16.867	11.479	14.216	1.00	14.85
20	ATOM	1987	CG	TYR A 256	0	17.883	10.349	14.316	1.00	13.96
	ATOM	1988	CD1	TYR A 256	0	19.030	10.427	13.529	1.00	13.97
	ATOM	1989	CD2	TYR A 256	0	17.712	9.245	15.129	1.00	14.62
	ATOM	1990	CE1	TYR A 256	0	19.986	9.422	13.534	1.00	13.83
	ATOM	1991	CE2	TYR A 256	0	18.667	8.224	15.170	1.00	15.31
25	ATOM	1992	CZ	TYR A 256	0	19.795	8.336	14.346	1.00	15.90
	ATOM	1993	OH	TYR A 256	0	20.763	7.341	14.337	1.00	17.15
	ATOM	1994	N	TRP A 257	0	13.801	12.198	13.564	1.00	13.58
	ATOM	1995	CA	TRP A 257	0	12.742	13.196	13.657	1.00	14.21
	ATOM	1996	C	TRP A 257	0	13.041	14.198	14.769	1.00	12.04
30	ATOM	1997	O	TRP A 257	0	13.382	13.811	15.878	1.00	10.46
	ATOM	1998	CB	TRP A 257	0	11.363	12.592	13.988	1.00	12.49
	ATOM	1999	CG	TRP A 257	0	10.648	11.906	12.865	1.00	13.06
	ATOM	2000	CD1	TRP A 257	0	10.315	10.568	12.879	1.00	12.86
	ATOM	2001	CD2	TRP A 257	0	10.161	12.437	11.633	1.00	12.33
35	ATOM	2002	NE1	TRP A 257	0	9.640	10.267	11.720	1.00	13.75
	ATOM	2003	CE2	TRP A 257	0	9.530	11.388	10.940	1.00	13.78
	ATOM	2004	CE3	TRP A 257	0	10.173	13.691	11.035	1.00	14.13
	ATOM	2005	CZ2	TRP A 257	0	8.940	11.538	9.681	1.00	13.24

	ATOM	2006	CZ3	TRP	A 257	0	9.590	13.868	9.786	1.00	14.34
	ATOM	2007	CH2	TRP	A 257	0	8.963	12.789	9.127	1.00	13.64
	ATOM	2008	N	ILE	A 258	0	12.790	15.463	14.454	1.00	12.29
	ATOM	2009	CA	ILE	A 258	0	12.886	16.498	15.508	1.00	12.44
5	ATOM	2010	C	ILE	A 258	0	11.391	16.840	15.769	1.00	12.40
	ATOM	2011	O	ILE	A 258	0	10.629	17.039	14.812	1.00	12.43
	ATOM	2012	CB	ILE	A 258	0	13.617	17.777	15.048	1.00	13.32
	ATOM	2013	CG1	ILE	A 258	0	15.107	17.477	14.854	1.00	14.52
	ATOM	2014	CG2	ILE	A 258	0	13.365	18.888	16.052	1.00	12.32
10	ATOM	2015	CD1	ILE	A 258	0	15.839	18.474	13.994	1.00	14.35
	ATOM	2016	N	ARG	A 259	0	11.017	16.764	17.013	1.00	11.51
	ATOM	2017	CA	ARG	A 259	0	9.610	16.832	17.407	1.00	13.43
	ATOM	2018	C	ARG	A 259	0	9.254	18.019	18.274	1.00	12.74
	ATOM	2019	O	ARG	A 259	0	9.931	18.246	19.280	1.00	12.62
15	ATOM	2020	CB	ARG	A 259	0	9.326	15.567	18.253	1.00	12.43
	ATOM	2021	CG	ARG	A 259	0	9.308	14.290	17.414	1.00	15.81
	ATOM	2022	CD	ARG	A 259	0	8.910	13.054	18.244	1.00	16.58
	ATOM	2023	NE	ARG	A 259	0	9.204	11.818	17.528	1.00	16.91
	ATOM	2024	CZ	ARG	A 259	0	8.475	11.187	16.616	1.00	18.43
20	ATOM	2025	NH1	ARG	A 259	0	7.285	11.657	16.239	1.00	19.39
	ATOM	2026	NH2	ARG	A 259	0	8.907	10.070	16.045	1.00	17.95
	ATOM	2027	N	ALA	A 260	0	8.226	18.764	17.884	1.00	13.12
	ATOM	2028	CA	ALA	A 260	0	7.768	19.882	18.727	1.00	12.65
	ATOM	2029	C	ALA	A 260	0	6.237	19.763	18.802	1.00	14.47
25	ATOM	2030	O	ALA	A 260	0	5.545	20.140	17.868	1.00	14.73
	ATOM	2031	CB	ALA	A 260	0	8.281	21.188	18.165	1.00	9.58
	ATOM	2032	N	GLN	A 261	0	5.690	19.225	19.870	1.00	14.78
	ATOM	2033	CA	GLN	A 261	0	4.272	19.004	20.060	1.00	16.99
	ATOM	2034	C	GLN	A 261	0	3.606	20.154	20.803	1.00	15.01
30	ATOM	2035	O	GLN	A 261	0	3.914	20.389	21.961	1.00	13.86
	ATOM	2036	CB	GLN	A 261	0	4.118	17.747	20.924	1.00	20.94
	ATOM	2037	CG	GLN	A 261	0	2.717	17.131	20.940	1.00	27.53
	ATOM	2038	CD	GLN	A 261	0	2.721	15.991	21.947	1.00	29.63
	ATOM	2039	OE1	GLN	A 261	0	3.152	14.887	21.682	1.00	31.60
35	ATOM	2040	NE2	GLN	A 261	0	2.331	16.255	23.188	1.00	34.91
	ATOM	2041	N	PRO	A 262	0	2.663	20.820	20.167	1.00	14.60
	ATOM	2042	CA	PRO	A 262	0	1.974	21.969	20.739	1.00	15.72
	ATOM	2043	C	PRO	A 262	0	0.921	21.568	21.757	1.00	16.25

	ATOM	2044	O	PRO A 262	0	0.498	20.409	21.814	1.00	15.61
	ATOM	2045	CB	PRO A 262	0	1.401	22.752	19.539	1.00	13.88
	ATOM	2046	CG	PRO A 262	0	1.168	21.608	18.563	1.00	13.62
	ATOM	2047	CD	PRO A 262	0	2.257	20.570	18.772	1.00	13.23
5	ATOM	2048	N	ASN A 263	0	0.570	22.481	22.665	1.00	17.25
	ATOM	2049	CA	ASN A 263	0	-0.471	22.203	23.648	1.00	17.50
	ATOM	2050	C	ASN A 263	0	-1.834	22.460	22.981	1.00	18.43
	ATOM	2051	O	ASN A 263	0	-2.810	22.121	23.608	1.00	19.35
	ATOM	2052	CB	ASN A 263	0	-0.422	22.990	24.954	1.00	16.12
10	ATOM	2053	CG	ASN A 263	0	-0.333	24.493	24.728	1.00	16.97
	ATOM	2054	OD1	ASN A 263	0	0.236	25.002	23.751	1.00	15.54
	ATOM	2055	ND2	ASN A 263	0	-0.905	25.269	25.653	1.00	16.31
	ATOM	2056	N	LYS A 264	0	-1.947	23.055	21.818	1.00	20.51
	ATOM	2057	CA	LYS A 264	0	-3.256	23.208	21.180	1.00	24.76
15	ATOM	2058	C	LYS A 264	0	-3.055	23.395	19.683	1.00	23.64
	ATOM	2059	O	LYS A 264	0	-1.909	23.572	19.267	1.00	24.23
	ATOM	2060	CB	LYS A 264	0	-4.038	24.393	21.775	1.00	25.87
	ATOM	2061	CG	LYS A 264	0	-3.266	25.702	21.602	1.00	28.62
	ATOM	2062	CD	LYS A 264	0	-3.579	26.624	22.772	1.00	30.65
20	ATOM	2063	CE	LYS A 264	0	-4.114	27.960	22.283	1.00	32.62
	ATOM	2064	NZ	LYS A 264	0	-4.593	28.753	23.459	1.00	34.39
	ATOM	2065	N	GLY A 265	0	-4.112	23.386	18.892	1.00	22.60
	ATOM	2066	CA	GLY A 265	0	-3.959	23.591	17.452	1.00	22.98
	ATOM	2067	C	GLY A 265	0	-5.190	23.002	16.758	1.00	23.95
25	ATOM	2068	O	GLY A 265	0	-5.904	22.202	17.362	1.00	22.64
	ATOM	2069	N	ARG A 266	0	-5.398	23.434	15.537	1.00	24.60
	ATOM	2070	CA	ARG A 266	0	-6.527	23.051	14.734	1.00	26.24
	ATOM	2071	C	ARG A 266	0	-6.412	21.605	14.272	1.00	27.29
	ATOM	2072	O	ARG A 266	0	-5.329	21.074	14.015	1.00	25.41
30	ATOM	2073	CB	ARG A 266	0	-6.628	23.903	13.469	1.00	30.71
	ATOM	2074	CG	ARG A 266	0	-7.065	25.334	13.563	1.00	35.66
	ATOM	2075	CD	ARG A 266	0	-8.161	25.673	12.539	1.00	40.48
	ATOM	2076	NE	ARG A 266	0	-9.379	25.957	13.286	1.00	45.08
	ATOM	2077	CZ	ARG A 266	0	-10.551	25.334	13.319	1.00	47.09
35	ATOM	2078	NH1	ARG A 266	0	-10.921	24.294	12.577	1.00	48.10
	ATOM	2079	NH2	ARG A 266	0	-11.452	25.828	14.165	1.00	47.80
	ATOM	2080	N	ASN A 267	0	-7.586	20.983	14.141	1.00	25.17
	ATOM	2081	CA	ASN A 267	0	-7.727	19.669	13.602	1.00	23.96

ATOM 2082 C ASN A 267 0 -6.859 18.625 14.244 1.00 22.35
ATOM 2083 O ASN A 267 0 -6.306 17.864 13.448 1.00 23.57
ATOM 2084 CB ASN A 267 0 -7.390 19.695 12.098 1.00 26.46
ATOM 2085 CG ASN A 267 0 -8.461 20.426 11.309 1.00 29.21
5 ATOM 2086 OD1 ASN A 267 0 -8.190 21.226 10.405 1.00 30.18
ATOM 2087 ND2 ASN A 267 0 -9.681 20.075 11.701 1.00 28.77
ATOM 2088 N GLY A 268 0 -6.706 18.594 15.550 1.00 21.85
ATOM 2089 CA GLY A 268 0 -5.890 17.533 16.121 1.00 22.47
ATOM 2090 C GLY A 268 0 -4.383 17.760 16.118 1.00 23.29
10 ATOM 2091 O GLY A 268 0 -3.652 16.898 16.632 1.00 23.28
ATOM 2092 N LEU A 269 0 -3.880 18.901 15.676 1.00 22.69
ATOM 2093 CA LEU A 269 0 -2.454 19.222 15.684 1.00 22.62
ATOM 2094 C LEU A 269 0 -1.753 18.890 16.990 1.00 23.26
ATOM 2095 O LEU A 269 0 -0.650 18.335 17.035 1.00 23.42
15 ATOM 2096 CB LEU A 269 0 -2.311 20.713 15.472 1.00 22.28
ATOM 2097 CG LEU A 269 0 -1.183 21.414 14.745 1.00 23.42
ATOM 2098 CD1 LEU A 269 0 -0.508 22.380 15.682 1.00 19.64
ATOM 2099 CD2 LEU A 269 0 -0.213 20.492 14.009 1.00 21.26
ATOM 2100 N ALA A 270 0 -2.371 19.199 18.135 1.00 21.51
20 ATOM 2101 CA ALA A 270 0 -1.784 18.899 19.419 1.00 22.26
ATOM 2102 C ALA A 270 0 -1.612 17.415 19.680 1.00 23.22
ATOM 2103 O ALA A 270 0 -0.898 17.077 20.637 1.00 21.81
ATOM 2104 CB ALA A 270 0 -2.632 19.518 20.542 1.00 21.06
ATOM 2105 N GLY A 271 0 -2.337 16.521 18.996 1.00 23.75
25 ATOM 2106 CA GLY A 271 0 -2.190 15.125 19.372 1.00 24.98
ATOM 2107 C GLY A 271 0 -1.507 14.267 18.328 1.00 26.07
ATOM 2108 O GLY A 271 0 -1.501 13.045 18.523 1.00 26.26
ATOM 2109 N THR A 272 0 -0.906 14.825 17.278 1.00 26.48
ATOM 2110 CA THR A 272 0 -0.327 13.901 16.294 1.00 25.27
30 ATOM 2111 C THR A 272 0 0.986 14.362 15.701 1.00 25.58
ATOM 2112 O THR A 272 0 1.216 15.567 15.701 1.00 24.46
ATOM 2113 CB THR A 272 0 -1.380 13.759 15.164 1.00 24.40
ATOM 2114 OG1 THR A 272 0 -0.931 12.737 14.275 1.00 26.32
ATOM 2115 CG2 THR A 272 0 -1.575 15.022 14.347 1.00 22.50
35 ATOM 2116 N PHE A 273 0 1.714 13.443 15.062 1.00 24.01
ATOM 2117 CA PHE A 273 0 2.897 13.755 14.271 1.00 23.99
ATOM 2118 C PHE A 273 0 2.663 13.201 12.858 1.00 24.84
ATOM 2119 O PHE A 273 0 3.534 13.207 11.987 1.00 24.73

	ATOM	2120	CB	PHE A 273	0	4.175	13.094	14.812	1.00	22.16
	ATOM	2121	CG	PHE A 273	0	4.550	13.676	16.153	1.00	21.84
	ATOM	2122	CD1	PHE A 273	0	4.190	13.037	17.327	1.00	20.67
	ATOM	2123	CD2	PHE A 273	0	5.221	14.881	16.216	1.00	20.98
5	ATOM	2124	CE1	PHE A 273	0	4.538	13.574	18.554	1.00	21.75
	ATOM	2125	CE2	PHE A 273	0	5.559	15.428	17.440	1.00	21.65
	ATOM	2126	CZ	PHE A 273	0	5.216	14.787	18.616	1.00	22.38
	ATOM	2127	N	ALA A 274	0	1.440	12.718	12.647	1.00	24.38
	ATOM	2128	CA	ALA A 274	0	1.094	12.053	11.397	1.00	24.29
10	ATOM	2129	C	ALA A 274	0	1.399	12.920	10.194	1.00	24.15
	ATOM	2130	O	ALA A 274	0	0.990	14.078	10.161	1.00	23.07
	ATOM	2131	CB	ALA A 274	0	-0.385	11.681	11.387	1.00	23.53
	ATOM	2132	N	ASN A 275	0	2.075	12.355	9.204	1.00	23.41
	ATOM	2133	CA	ASN A 275	0	2.389	13.068	7.987	1.00	24.88
15	ATOM	2134	C	ASN A 275	0	3.498	14.093	8.191	1.00	22.73
	ATOM	2135	O	ASN A 275	0	3.708	14.947	7.337	1.00	21.57
	ATOM	2136	CB	ASN A 275	0	1.138	13.806	7.516	1.00	30.04
	ATOM	2137	CG	ASN A 275	0	0.194	13.070	6.633	1.00	35.28
	ATOM	2138	OD1	ASN A 275	0	-0.458	12.071	6.985	1.00	36.92
20	ATOM	2139	ND2	ASN A 275	0	0.156	13.655	5.427	1.00	37.87
	ATOM	2140	N	GLY A 276	0	4.185	14.083	9.322	1.00	22.10
	ATOM	2141	CA	GLY A 276	0	5.278	15.025	9.503	1.00	20.95
	ATOM	2142	C	GLY A 276	0	4.801	16.392	9.962	1.00	19.61
	ATOM	2143	O	GLY A 276	0	5.587	17.325	9.816	1.00	19.96
25	ATOM	2144	N	VAL A 277	0	3.600	16.504	10.540	1.00	16.82
	ATOM	2145	CA	VAL A 277	0	3.207	17.796	11.107	1.00	15.06
	ATOM	2146	C	VAL A 277	0	4.033	17.942	12.379	1.00	13.80
	ATOM	2147	O	VAL A 277	0	4.454	16.912	12.926	1.00	13.80
	ATOM	2148	CB	VAL A 277	0	1.676	17.849	11.397	1.00	14.37
30	ATOM	2149	CG1	VAL A 277	0	0.882	17.824	10.099	1.00	13.37
	ATOM	2150	CG2	VAL A 277	0	1.213	16.763	12.330	1.00	11.77
	ATOM	2151	N	ASN A 278	0	4.307	19.100	12.936	1.00	14.25
	ATOM	2152	CA	ASN A 278	0	5.026	19.262	14.209	1.00	13.80
	ATOM	2153	C	ASN A 278	0	6.443	18.640	14.208	1.00	13.80
35	ATOM	2154	O	ASN A 278	0	7.020	18.228	15.229	1.00	11.81
	ATOM	2155	CB	ASN A 278	0	4.216	18.607	15.312	1.00	14.24
	ATOM	2156	CG	ASN A 278	0	2.890	19.288	15.659	1.00	15.35
	ATOM	2157	OD1	ASN A 278	0	1.952	18.531	16.009	1.00	14.81

	ATOM	2158	ND2	ASN	A 278	0	2.821	20.591	15.593	1.00	10.69
	ATOM	2159	N	SER	A 279	0	7.044	18.595	13.025	1.00	12.68
	ATOM	2160	CA	SER	A 279	0	8.296	17.892	12.860	1.00	15.48
	ATOM	2161	C	SER	A 279	0	9.323	18.571	11.964	1.00	15.07
5	ATOM	2162	O	SER	A 279	0	8.995	19.309	11.044	1.00	12.20
	ATOM	2163	CB	SER	A 279	0	7.976	16.549	12.122	1.00	14.76
	ATOM	2164	OG	SER	A 279	0	7.268	15.722	13.054	1.00	19.57
	ATOM	2165	N	ALA	A 280	0	10.570	18.152	12.229	1.00	15.67
	ATOM	2166	CA	ALA	A 280	0	11.664	18.548	11.327	1.00	16.75
10	ATOM	2167	C	ALA	A 280	0	12.620	17.341	11.287	1.00	15.83
	ATOM	2168	O	ALA	A 280	0	12.438	16.346	11.997	1.00	15.55
	ATOM	2169	CB	ALA	A 280	0	12.363	19.828	11.745	1.00	16.40
	ATOM	2170	N	ILE	A 281	0	13.669	17.478	10.485	1.00	14.79
	ATOM	2171	CA	ILE	A 281	0	14.569	16.346	10.257	1.00	15.55
15	ATOM	2172	C	ILE	A 281	0	16.002	16.610	10.699	1.00	15.92
	ATOM	2173	O	ILE	A 281	0	16.649	17.577	10.284	1.00	14.96
	ATOM	2174	CB	ILE	A 281	0	14.557	16.013	8.735	1.00	16.44
	ATOM	2175	CG1	ILE	A 281	0	13.147	15.573	8.275	1.00	16.42
	ATOM	2176	CG2	ILE	A 281	0	15.615	14.959	8.421	1.00	15.71
20	ATOM	2177	CD1	ILE	A 281	0	12.981	15.376	6.771	1.00	14.22
	ATOM	2178	N	LEU	A 282	0	16.505	15.698	11.515	1.00	16.76
	ATOM	2179	CA	LEU	A 282	0	17.920	15.736	11.912	1.00	15.82
	ATOM	2180	C	LEU	A 282	0	18.655	14.747	10.990	1.00	16.16
	ATOM	2181	O	LEU	A 282	0	18.409	13.530	11.034	1.00	16.41
25	ATOM	2182	CB	LEU	A 282	0	18.129	15.400	13.379	1.00	14.54
	ATOM	2183	CG	LEU	A 282	0	19.632	15.346	13.773	1.00	16.00
	ATOM	2184	CD1	LEU	A 282	0	20.100	16.767	14.052	1.00	16.10
	ATOM	2185	CD2	LEU	A 282	0	19.865	14.469	14.970	1.00	13.21
	ATOM	2186	N	ARG	A 283	0	19.490	15.254	10.100	1.00	15.20
30	ATOM	2187	CA	ARG	A 283	0	20.160	14.377	9.141	1.00	16.98
	ATOM	2188	C	ARG	A 283	0	21.683	14.326	9.279	1.00	17.31
	ATOM	2189	O	ARG	A 283	0	22.398	15.330	9.203	1.00	17.82
	ATOM	2190	CB	ARG	A 283	0	19.844	14.861	7.736	1.00	17.30
	ATOM	2191	CG	ARG	A 283	0	20.417	13.978	6.641	1.00	19.94
35	ATOM	2192	CD	ARG	A 283	0	19.860	14.446	5.301	1.00	20.04
	ATOM	2193	NE	ARG	A 283	0	18.474	14.010	5.208	1.00	21.56
	ATOM	2194	CZ	ARG	A 283	0	17.479	14.530	4.505	1.00	21.81
	ATOM	2195	NH1	ARG	A 283	0	16.287	13.922	4.564	1.00	21.52

	ATOM	2196	NH2	ARG	A	283	0	17.653	15.634	3.797	1.00	21.84
	ATOM	2197	N	TYR	A	284	0	22.163	13.136	9.567	1.00	16.79
	ATOM	2198	CA	TYR	A	284	0	23.581	12.821	9.620	1.00	16.35
	ATOM	2199	C	TYR	A	284	0	24.155	12.787	8.198	1.00	16.52
5	ATOM	2200	O	TYR	A	284	0	23.556	12.226	7.271	1.00	16.33
	ATOM	2201	CB	TYR	A	284	0	23.730	11.444	10.252	1.00	16.51
	ATOM	2202	CG	TYR	A	284	0	23.727	11.460	11.755	1.00	17.09
	ATOM	2203	CD1	TYR	A	284	0	24.910	11.178	12.437	1.00	17.37
	ATOM	2204	CD2	TYR	A	284	0	22.601	11.753	12.504	1.00	17.15
10	ATOM	2205	CE1	TYR	A	284	0	24.937	11.163	13.817	1.00	17.64
	ATOM	2206	CE2	TYR	A	284	0	22.623	11.770	13.892	1.00	15.66
	ATOM	2207	CZ	TYR	A	284	0	23.796	11.476	14.542	1.00	15.99
	ATOM	2208	OH	TYR	A	284	0	23.873	11.448	15.919	1.00	14.03
	ATOM	2209	N	ALA	A	285	0	25.276	13.463	7.992	1.00	17.42
15	ATOM	2210	CA	ALA	A	285	0	25.950	13.461	6.692	1.00	19.35
	ATOM	2211	C	ALA	A	285	0	26.186	11.994	6.328	1.00	19.20
	ATOM	2212	O	ALA	A	285	0	26.692	11.237	7.146	1.00	17.18
	ATOM	2213	CB	ALA	A	285	0	27.293	14.194	6.770	1.00	19.86
	ATOM	2214	N	GLY	A	286	0	25.724	11.614	5.153	1.00	20.01
20	ATOM	2215	CA	GLY	A	286	0	25.851	10.224	4.747	1.00	21.88
	ATOM	2216	C	GLY	A	286	0	24.507	9.510	4.754	1.00	22.87
	ATOM	2217	O	GLY	A	286	0	24.406	8.418	4.197	1.00	23.06
	ATOM	2218	N	ALA	A	287	0	23.504	10.076	5.423	1.00	22.81
	ATOM	2219	CA	ALA	A	287	0	22.176	9.449	5.364	1.00	21.50
25	ATOM	2220	C	ALA	A	287	0	21.482	9.880	4.079	1.00	20.58
	ATOM	2221	O	ALA	A	287	0	21.647	11.032	3.629	1.00	19.44
	ATOM	2222	CB	ALA	A	287	0	21.340	9.890	6.562	1.00	21.34
	ATOM	2223	N	ALA	A	288	0	20.632	9.041	3.523	1.00	21.20
	ATOM	2224	CA	ALA	A	288	0	19.899	9.450	2.310	1.00	23.46
30	ATOM	2225	C	ALA	A	288	0	18.965	10.629	2.513	1.00	24.70
	ATOM	2226	O	ALA	A	288	0	18.494	10.929	3.621	1.00	25.30
	ATOM	2227	CB	ALA	A	288	0	19.012	8.298	1.827	1.00	24.84
	ATOM	2228	N	ASN	A	289	0	18.638	11.300	1.411	1.00	25.98
	ATOM	2229	CA	ASN	A	289	0	17.674	12.398	1.439	1.00	27.16
35	ATOM	2230	C	ASN	A	289	0	16.303	11.707	1.505	1.00	27.36
	ATOM	2231	O	ASN	A	289	0	15.761	11.330	0.477	1.00	27.56
	ATOM	2232	CB	ASN	A	289	0	17.784	13.250	0.189	1.00	29.01
	ATOM	2233	CG	ASN	A	289	0	18.808	14.364	0.299	1.00	30.44

	ATOM	2234	OD1	ASN	A 289	0	20.005	14.168	0.545	1.00	30.40
	ATOM	2235	ND2	ASN	A 289	0	18.340	15.591	0.121	1.00	31.98
	ATOM	2236	N	ALA	A 290	0	15.837	11.426	2.703	1.00	25.22
	ATOM	2237	CA	ALA	A 290	0	14.600	10.727	2.955	1.00	25.09
5	ATOM	2238	C	ALA	A 290	0	14.087	11.057	4.363	1.00	22.98
	ATOM	2239	O	ALA	A 290	0	14.830	11.555	5.205	1.00	22.02
	ATOM	2240	CB	ALA	A 290	0	14.764	9.210	2.823	1.00	24.89
	ATOM	2241	N	ASP	A 291	0	12.822	10.718	4.597	1.00	21.88
	ATOM	2242	CA	ASP	A 291	0	12.223	10.985	5.907	1.00	21.71
10	ATOM	2243	C	ASP	A 291	0	12.724	9.965	6.916	1.00	18.93
	ATOM	2244	O	ASP	A 291	0	12.911	8.814	6.596	1.00	19.66
	ATOM	2245	CB	ASP	A 291	0	10.695	10.862	5.834	1.00	22.63
	ATOM	2246	CG	ASP	A 291	0	10.088	12.005	5.076	1.00	25.41
	ATOM	2247	OD1	ASP	A 291	0	10.781	12.988	4.735	1.00	27.11
15	ATOM	2248	OD2	ASP	A 291	0	8.885	11.932	4.812	1.00	27.47
	ATOM	2249	N	PRO	A 292	0	12.863	10.362	8.164	1.00	16.14
	ATOM	2250	CA	PRO	A 292	0	13.229	9.473	9.230	1.00	15.27
	ATOM	2251	C	PRO	A 292	0	12.087	8.484	9.389	1.00	19.40
	ATOM	2252	O	PRO	A 292	0	10.925	8.785	9.063	1.00	20.36
20	ATOM	2253	CB	PRO	A 292	0	13.257	10.335	10.511	1.00	14.68
	ATOM	2254	CG	PRO	A 292	0	13.291	11.739	9.941	1.00	14.39
	ATOM	2255	CD	PRO	A 292	0	12.606	11.735	8.593	1.00	14.02
	ATOM	2256	N	THR	A 293	0	12.357	7.361	10.024	1.00	19.91
	ATOM	2257	CA	THR	A 293	0	11.360	6.379	10.373	1.00	20.62
25	ATOM	2258	C	THR	A 293	0	11.589	6.055	11.847	1.00	20.83
	ATOM	2259	O	THR	A 293	0	11.323	4.943	12.287	1.00	23.91
	ATOM	2260	CB	THR	A 293	0	11.556	5.088	9.557	1.00	23.41
	ATOM	2261	OG1	THR	A 293	0	12.874	4.577	9.836	1.00	24.50
	ATOM	2262	CG2	THR	A 293	0	11.438	5.341	8.058	1.00	23.72
30	ATOM	2263	N	THR	A 294	0	12.172	6.958	12.624	1.00	19.30
	ATOM	2264	CA	THR	A 294	0	12.440	6.634	14.017	1.00	19.42
	ATOM	2265	C	THR	A 294	0	11.214	6.896	14.878	1.00	20.66
	ATOM	2266	O	THR	A 294	0	10.240	7.485	14.411	1.00	19.89
	ATOM	2267	CB	THR	A 294	0	13.565	7.548	14.553	1.00	19.28
35	ATOM	2268	OG1	THR	A 294	0	13.174	8.889	14.251	1.00	17.55
	ATOM	2269	CG2	THR	A 294	0	14.860	7.214	13.822	1.00	19.27
	ATOM	2270	N	SER	A 295	0	11.359	6.576	16.159	1.00	23.85
	ATOM	2271	CA	SER	A 295	0	10.274	6.851	17.095	1.00	27.18

	ATOM	2272	C	SER A 295	0	10.781	7.484	18.375	1.00	27.92
	ATOM	2273	O	SER A 295	0	11.900	7.292	18.844	1.00	27.09
	ATOM	2274	CB	SER A 295	0	9.513	5.546	17.367	1.00	28.92
	ATOM	2275	OG	SER A 295	0	10.389	4.761	18.160	1.00	33.04
5	ATOM	2276	N	ALA A 296	0	9.930	8.331	18.965	1.00	30.04
	ATOM	2277	CA	ALA A 296	0	10.295	9.003	20.207	1.00	29.82
	ATOM	2278	C	ALA A 296	0	10.552	8.011	21.327	1.00	30.83
	ATOM	2279	O	ALA A 296	0	10.114	6.861	21.328	1.00	30.67
	ATOM	2280	CB	ALA A 296	0	9.187	9.968	20.599	1.00	30.16
10	ATOM	2281	N	ASN A 297	0	11.286	8.489	22.328	1.00	31.65
	ATOM	2282	CA	ASN A 297	0	11.543	7.750	23.549	1.00	32.16
	ATOM	2283	C	ASN A 297	0	10.200	7.650	24.285	1.00	32.80
	ATOM	2284	O	ASN A 297	0	9.492	8.616	24.565	1.00	31.30
	ATOM	2285	CB	ASN A 297	0	12.522	8.497	24.443	1.00	33.07
15	ATOM	2286	CG	ASN A 297	0	12.869	7.742	25.706	1.00	35.21
	ATOM	2287	OD1	ASN A 297	0	12.116	6.965	26.284	1.00	35.45
	ATOM	2288	ND2	ASN A 297	0	14.106	7.982	26.162	1.00	37.10
	ATOM	2289	N	PRO A 298	0	9.865	6.430	24.647	1.00	33.40
	ATOM	2290	CA	PRO A 298	0	8.626	6.116	25.331	1.00	33.89
20	ATOM	2291	C	PRO A 298	0	8.580	6.690	26.732	1.00	32.60
	ATOM	2292	O	PRO A 298	0	7.522	7.155	27.173	1.00	32.72
	ATOM	2293	CB	PRO A 298	0	8.505	4.576	25.358	1.00	35.13
	ATOM	2294	CG	PRO A 298	0	9.932	4.147	25.128	1.00	34.52
	ATOM	2295	CD	PRO A 298	0	10.630	5.222	24.323	1.00	34.10
25	ATOM	2296	N	ASN A 299	0	9.689	6.721	27.461	1.00	29.60
	ATOM	2297	CA	ASN A 299	0	9.701	7.229	28.834	1.00	28.47
	ATOM	2298	C	ASN A 299	0	10.818	8.251	29.006	1.00	27.18
	ATOM	2299	O	ASN A 299	0	11.906	7.967	29.528	1.00	25.69
	ATOM	2300	CB	ASN A 299	0	9.964	6.017	29.747	1.00	29.50
30	ATOM	2301	CG	ASN A 299	0	8.907	4.935	29.673	1.00	32.34
	ATOM	2302	OD1	ASN A 299	0	9.090	3.873	29.075	1.00	33.50
	ATOM	2303	ND2	ASN A 299	0	7.735	5.182	30.251	1.00	33.04
	ATOM	2304	N	PRO A 300	0	10.629	9.450	28.498	1.00	26.02
	ATOM	2305	CA	PRO A 300	0	11.668	10.486	28.498	1.00	23.99
35	ATOM	2306	C	PRO A 300	0	11.987	11.054	29.860	1.00	21.16
	ATOM	2307	O	PRO A 300	0	11.051	11.174	30.649	1.00	20.81
	ATOM	2308	CB	PRO A 300	0	11.137	11.623	27.594	1.00	23.33
	ATOM	2309	CG	PRO A 300	0	9.645	11.422	27.729	1.00	24.68

	ATOM	2310	CD	PRO	A	300	0	9.387	9.918	27.882	1.00	25.22
	ATOM	2311	N	ALA	A	301	0	13.242	11.361	30.179	1.00	19.17
	ATOM	2312	CA	ALA	A	301	0	13.538	12.139	31.410	1.00	17.57
	ATOM	2313	C	ALA	A	301	0	13.159	13.588	31.084	1.00	16.53
5	ATOM	2314	O	ALA	A	301	0	13.613	14.235	30.131	1.00	16.24
	ATOM	2315	CB	ALA	A	301	0	15.006	11.982	31.774	1.00	17.17
	ATOM	2316	N	GLN	A	302	0	12.139	14.131	31.723	1.00	18.15
	ATOM	2317	CA	GLN	A	302	0	11.580	15.446	31.441	1.00	19.34
	ATOM	2318	C	GLN	A	302	0	12.335	16.580	32.124	1.00	19.16
10	ATOM	2319	O	GLN	A	302	0	12.577	16.444	33.324	1.00	19.07
	ATOM	2320	CB	GLN	A	302	0	10.122	15.483	31.937	1.00	19.10
	ATOM	2321	CG	GLN	A	302	0	9.304	16.666	31.478	1.00	20.55
	ATOM	2322	CD	GLN	A	302	0	8.960	16.738	30.009	1.00	20.18
	ATOM	2323	OE1	GLN	A	302	0	8.843	15.721	29.331	1.00	22.29
15	ATOM	2324	NE2	GLN	A	302	0	8.813	17.936	29.436	1.00	18.46
	ATOM	2325	N	LEU	A	303	0	12.629	17.681	31.444	1.00	17.92
	ATOM	2326	CA	LEU	A	303	0	13.241	18.824	32.139	1.00	17.32
	ATOM	2327	C	LEU	A	303	0	12.316	19.357	33.232	1.00	17.65
	ATOM	2328	O	LEU	A	303	0	11.140	19.664	33.021	1.00	17.55
20	ATOM	2329	CB	LEU	A	303	0	13.489	19.988	31.168	1.00	15.14
	ATOM	2330	CG	LEU	A	303	0	13.919	21.317	31.797	1.00	16.94
	ATOM	2331	CD1	LEU	A	303	0	15.262	21.146	32.504	1.00	17.30
	ATOM	2332	CD2	LEU	A	303	0	13.988	22.432	30.764	1.00	12.82
	ATOM	2333	N	ASN	A	304	0	12.868	19.580	34.399	1.00	17.34
25	ATOM	2334	CA	ASN	A	304	0	12.199	20.212	35.531	1.00	19.12
	ATOM	2335	C	ASN	A	304	0	13.071	21.435	35.833	1.00	19.06
	ATOM	2336	O	ASN	A	304	0	14.265	21.349	36.122	1.00	20.37
	ATOM	2337	CB	ASN	A	304	0	12.073	19.244	36.704	1.00	22.16
	ATOM	2338	CG	ASN	A	304	0	11.748	19.900	38.024	1.00	25.02
30	ATOM	2339	OD1	ASN	A	304	0	11.506	21.111	38.146	1.00	26.72
	ATOM	2340	ND2	ASN	A	304	0	11.766	19.133	39.114	1.00	25.99
	ATOM	2341	N	GLU	A	305	0	12.541	22.629	35.662	1.00	17.64
	ATOM	2342	CA	GLU	A	305	0	13.204	23.890	35.840	1.00	16.64
	ATOM	2343	C	GLU	A	305	0	13.884	23.977	37.194	1.00	16.06
35	ATOM	2344	O	GLU	A	305	0	14.965	24.564	37.208	1.00	14.78
	ATOM	2345	CB	GLU	A	305	0	12.286	25.085	35.567	1.00	15.91
	ATOM	2346	CG	GLU	A	305	0	12.898	26.484	35.831	1.00	14.81
	ATOM	2347	CD	GLU	A	305	0	11.794	27.546	35.666	1.00	15.72

ATOM 2348 OE1 GLU A 305 O 11.584 28.026 34.527 1.00 14.63
ATOM 2349 OE2 GLU A 305 O 11.154 27.861 36.685 1.00 13.05
ATOM 2350 N ALA A 306 O 13.416 23.432 38.298 1.00 15.83
ATOM 2351 CA ALA A 306 O 14.131 23.509 39.565 1.00 17.92
5 ATOM 2352 C ALA A 306 O 15.437 22.682 39.532 1.00 18.62
ATOM 2353 O ALA A 306 O 16.213 22.867 40.464 1.00 18.37
ATOM 2354 CB ALA A 306 O 13.283 22.993 40.711 1.00 16.23
ATOM 2355 N ASP A 307 O 15.721 21.860 38.523 1.00 18.04
ATOM 2356 CA ASP A 307 O 16.988 21.164 38.409 1.00 18.68
10 ATOM 2357 C ASP A 307 O 18.035 22.039 37.707 1.00 19.89
ATOM 2358 O ASP A 307 O 19.239 21.695 37.739 1.00 20.36
ATOM 2359 CB ASP A 307 O 16.904 19.863 37.592 1.00 17.64
ATOM 2360 CG ASP A 307 O 15.980 18.873 38.290 1.00 18.17
ATOM 2361 OD1 ASP A 307 O 15.918 18.919 39.535 1.00 18.27
15 ATOM 2362 OD2 ASP A 307 O 15.311 18.094 37.592 1.00 17.32
ATOM 2363 N LEU A 308 O 17.583 23.110 37.052 1.00 16.43
ATOM 2364 CA LEU A 308 O 18.581 23.962 36.377 1.00 16.80
ATOM 2365 C LEU A 308 O 19.327 24.827 37.384 1.00 16.94
ATOM 2366 O LEU A 308 O 18.784 25.320 38.380 1.00 17.28
20 ATOM 2367 CB LEU A 308 O 17.925 24.775 35.257 1.00 12.52
ATOM 2368 CG LEU A 308 O 17.436 23.936 34.073 1.00 12.15
ATOM 2369 CD1 LEU A 308 O 16.692 24.834 33.101 1.00 11.67
ATOM 2370 CD2 LEU A 308 O 18.547 23.186 33.341 1.00 12.23
ATOM 2371 N HIS A 309 O 20.640 24.968 37.243 1.00 18.01
25 ATOM 2372 CA HIS A 309 O 21.430 25.802 38.158 1.00 18.47
ATOM 2373 C HIS A 309 O 22.328 26.770 37.394 1.00 17.36
ATOM 2374 O HIS A 309 O 23.015 26.378 36.459 1.00 17.82
ATOM 2375 CB HIS A 309 O 22.267 24.997 39.140 1.00 18.51
ATOM 2376 CG HIS A 309 O 21.470 24.052 39.965 1.00 20.71
30 ATOM 2377 ND1 HIS A 309 O 21.526 22.684 39.790 1.00 21.77
ATOM 2378 CD2 HIS A 309 O 20.578 24.285 40.956 1.00 22.07
ATOM 2379 CE1 HIS A 309 O 20.701 22.115 40.657 1.00 22.85
ATOM 2380 NE2 HIS A 309 O 20.120 23.059 41.377 1.00 22.67
ATOM 2381 N ALA A 310 O 22.352 28.005 37.837 1.00 17.27
35 ATOM 2382 CA ALA A 310 O 23.173 29.068 37.228 1.00 17.74
ATOM 2383 C ALA A 310 O 24.663 28.775 37.342 1.00 18.13
ATOM 2384 O ALA A 310 O 25.103 28.233 38.369 1.00 19.61
ATOM 2385 CB ALA A 310 O 22.869 30.356 37.985 1.00 16.92

ATOM 2386 N LEU A 311 O 25.427 29.021 36.304 1.00 19.30
ATOM 2387 CA LEU A 311 O 26.856 28.762 36.277 1.00 20.71
ATOM 2388 C LEU A 311 O 27.655 29.922 36.881 1.00 22.67
ATOM 2389 O LEU A 311 O 28.581 29.788 37.682 1.00 23.06
5 ATOM 2390 CB LEU A 311 O 27.305 28.591 34.817 1.00 20.57
ATOM 2391 CG LEU A 311 O 28.796 28.196 34.684 1.00 21.52
ATOM 2392 CD1 LEU A 311 O 28.993 26.783 35.229 1.00 20.80
ATOM 2393 CD2 LEU A 311 O 29.319 28.282 33.254 1.00 20.17
ATOM 2394 N ILE A 312 O 27.333 31.142 36.449 1.00 23.42
10 ATOM 2395 CA ILE A 312 O 28.092 32.311 36.899 1.00 24.86
ATOM 2396 C ILE A 312 O 27.337 33.157 37.914 1.00 26.54
ATOM 2397 O ILE A 312 O 26.154 33.467 37.739 1.00 25.31
ATOM 2398 CB ILE A 312 O 28.397 33.179 35.670 1.00 24.45
ATOM 2399 CG1 ILE A 312 O 28.998 32.330 34.576 1.00 25.60
15 ATOM 2400 CG2 ILE A 312 O 29.261 34.373 36.075 1.00 26.44
ATOM 2401 CD1 ILE A 312 O 30.462 32.026 34.512 1.00 24.51
ATOM 2402 N ASP A 313 O 28.008 33.523 39.003 1.00 28.70
ATOM 2403 CA ASP A 313 O 27.432 34.339 40.071 1.00 30.99
ATOM 2404 C ASP A 313 O 26.065 33.763 40.417 1.00 29.83
20 ATOM 2405 O ASP A 313 O 25.024 34.385 40.235 1.00 28.51
ATOM 2406 CB ASP A 313 O 27.266 35.777 39.576 1.00 35.88
ATOM 2407 CG ASP A 313 O 28.532 36.505 39.187 1.00 40.21
ATOM 2408 OD1 ASP A 313 O 29.577 36.243 39.847 1.00 42.99
ATOM 2409 OD2 ASP A 313 O 28.525 37.346 38.252 1.00 40.95
25 ATOM 2410 N PRO A 314 O 26.041 32.517 40.863 1.00 28.77
ATOM 2411 CA PRO A 314 O 24.841 31.743 41.074 1.00 27.80
ATOM 2412 C PRO A 314 O 23.865 32.198 42.137 1.00 26.49
ATOM 2413 O PRO A 314 O 22.671 31.857 42.032 1.00 27.17
ATOM 2414 CB PRO A 314 O 25.297 30.311 41.479 1.00 27.61
30 ATOM 2415 CG PRO A 314 O 26.711 30.573 41.929 1.00 29.37
ATOM 2416 CD PRO A 314 O 27.248 31.726 41.111 1.00 28.10
ATOM 2417 N ALA A 315 O 24.364 32.818 43.206 1.00 23.45
ATOM 2418 CA ALA A 315 O 23.505 33.092 44.336 1.00 22.34
ATOM 2419 C ALA A 315 O 22.414 34.111 44.008 1.00 22.46
35 ATOM 2420 O ALA A 315 O 22.678 35.127 43.370 1.00 22.52
ATOM 2421 CB ALA A 315 O 24.294 33.617 45.532 1.00 21.68
ATOM 2422 N ALA A 316 O 21.226 33.838 44.534 1.00 20.85
ATOM 2423 CA ALA A 316 O 20.133 34.805 44.422 1.00 20.78

ATOM 2424 C ALA A 316 O 20.547 36.010 45.271 1.00 20.55
ATOM 2425 O ALA A 316 O 21.143 35.846 46.333 1.00 21.47
ATOM 2426 CB ALA A 316 O 18.897 34.166 45.043 1.00 18.32
ATOM 2427 N PRO A 317 O 20.237 37.212 44.864 1.00 20.84
5 ATOM 2428 CA PRO A 317 O 20.539 38.410 45.634 1.00 20.82
ATOM 2429 C PRO A 317 O 19.766 38.449 46.945 1.00 20.96
ATOM 2430 O PRO A 317 O 18.668 37.885 47.030 1.00 21.42
ATOM 2431 CB PRO A 317 O 20.064 39.590 44.758 1.00 21.64
ATOM 2432 CG PRO A 317 O 19.178 38.938 43.746 1.00 21.69
10 ATOM 2433 CD PRO A 317 O 19.517 37.466 43.619 1.00 20.10
ATOM 2434 N GLY A 318 O 20.269 39.080 47.988 1.00 20.69
ATOM 2435 CA GLY A 318 O 19.533 39.282 49.225 1.00 21.68
ATOM 2436 C GLY A 318 O 19.631 38.218 50.283 1.00 22.93
ATOM 2437 O GLY A 318 O 20.344 37.221 50.101 1.00 23.87
15 ATOM 2438 N ILE A 319 O 18.895 38.398 51.368 1.00 22.20
ATOM 2439 CA ILE A 319 O 18.879 37.432 52.454 1.00 24.16
ATOM 2440 C ILE A 319 O 18.169 36.189 51.956 1.00 25.28
ATOM 2441 O ILE A 319 O 17.071 36.271 51.405 1.00 26.26
ATOM 2442 CB ILE A 319 O 18.208 38.030 53.704 1.00 24.54
20 ATOM 2443 CG1 ILE A 319 O 19.075 39.176 54.213 1.00 25.08
ATOM 2444 CG2 ILE A 319 O 17.944 37.012 54.793 1.00 24.03
ATOM 2445 CD1 ILE A 319 O 18.262 40.183 55.006 1.00 27.56
ATOM 2446 N PRO A 320 O 18.762 35.030 52.159 1.00 26.23
ATOM 2447 CA PRO A 320 O 18.273 33.748 51.684 1.00 26.64
25 ATOM 2448 C PRO A 320 O 17.105 33.172 52.453 1.00 26.74
ATOM 2449 O PRO A 320 O 17.140 32.025 52.896 1.00 27.54
ATOM 2450 CB PRO A 320 O 19.501 32.801 51.772 1.00 27.16
ATOM 2451 CG PRO A 320 O 20.216 33.388 52.985 1.00 25.20
ATOM 2452 CD PRO A 320 O 20.061 34.891 52.837 1.00 25.62
30 ATOM 2453 N THR A 321 O 16.022 33.909 52.611 1.00 27.35
ATOM 2454 CA THR A 321 O 14.820 33.550 53.329 1.00 28.07
ATOM 2455 C THR A 321 O 13.632 34.190 52.603 1.00 27.48
ATOM 2456 O THR A 321 O 13.597 35.383 52.302 1.00 27.13
ATOM 2457 CB THR A 321 O 14.824 34.085 54.780 1.00 29.87
35 ATOM 2458 OG1 THR A 321 O 15.957 33.582 55.511 1.00 31.85
ATOM 2459 CG2 THR A 321 O 13.548 33.687 55.507 1.00 31.06
ATOM 2460 N PRO A 322 O 12.630 33.378 52.326 1.00 26.63
ATOM 2461 CA PRO A 322 O 11.428 33.824 51.637 1.00 25.91

	ATOM	2462	C	PRO A 322	0	10.892	35.072	52.313	1.00	25.37
	ATOM	2463	O	PRO A 322	0	10.945	35.194	53.542	1.00	25.02
	ATOM	2464	CB	PRO A 322	0	10.456	32.638	51.661	1.00	26.11
	ATOM	2465	CG	PRO A 322	0	11.370	31.477	51.931	1.00	26.67
5	ATOM	2466	CD	PRO A 322	0	12.592	31.961	52.691	1.00	26.21
	ATOM	2467	N	GLY A 323	0	10.432	36.075	51.573	1.00	24.30
	ATOM	2468	CA	GLY A 323	0	9.943	37.288	52.197	1.00	24.13
	ATOM	2469	C	GLY A 323	0	11.013	38.161	52.842	1.00	25.48
	ATOM	2470	O	GLY A 323	0	10.603	39.128	53.512	1.00	25.28
10	ATOM	2471	N	ALA A 324	0	12.320	37.959	52.688	1.00	24.80
	ATOM	2472	CA	ALA A 324	0	13.278	38.831	53.377	1.00	24.61
	ATOM	2473	C	ALA A 324	0	14.034	39.773	52.451	1.00	23.92
	ATOM	2474	O	ALA A 324	0	15.148	40.225	52.748	1.00	24.53
	ATOM	2475	CB	ALA A 324	0	14.255	38.012	54.204	1.00	23.79
15	ATOM	2476	N	ALA A 325	0	13.423	40.081	51.315	1.00	22.22
	ATOM	2477	CA	ALA A 325	0	14.033	40.985	50.341	1.00	20.42
	ATOM	2478	C	ALA A 325	0	13.825	42.423	50.803	1.00	19.97
	ATOM	2479	O	ALA A 325	0	12.987	42.648	51.677	1.00	18.14
	ATOM	2480	CB	ALA A 325	0	13.272	40.763	49.018	1.00	19.40
20	ATOM	2481	N	ASP A 326	0	14.422	43.421	50.161	1.00	20.69
	ATOM	2482	CA	ASP A 326	0	14.141	44.804	50.529	1.00	22.54
	ATOM	2483	C	ASP A 326	0	12.702	45.158	50.220	1.00	22.83
	ATOM	2484	O	ASP A 326	0	12.015	45.754	51.030	1.00	23.68
	ATOM	2485	CB	ASP A 326	0	15.089	45.767	49.789	1.00	22.32
25	ATOM	2486	CG	ASP A 326	0	16.494	45.378	50.238	1.00	23.83
	ATOM	2487	OD1	ASP A 326	0	16.650	45.284	51.475	1.00	24.78
	ATOM	2488	OD2	ASP A 326	0	17.393	45.171	49.409	1.00	24.90
	ATOM	2489	N	VAL A 327	0	12.254	44.821	49.026	1.00	24.29
	ATOM	2490	CA	VAL A 327	0	10.914	45.064	48.503	1.00	23.57
30	ATOM	2491	C	VAL A 327	0	10.246	43.721	48.170	1.00	23.46
	ATOM	2492	O	VAL A 327	0	10.785	42.933	47.386	1.00	22.62
	ATOM	2493	CB	VAL A 327	0	10.946	45.898	47.220	1.00	24.70
	ATOM	2494	CG1	VAL A 327	0	9.554	46.274	46.751	1.00	24.11
	ATOM	2495	CG2	VAL A 327	0	11.773	47.173	47.420	1.00	26.30
35	ATOM	2496	N	ASN A 328	0	9.113	43.463	48.811	1.00	21.44
	ATOM	2497	CA	ASN A 328	0	8.390	42.212	48.717	1.00	23.21
	ATOM	2498	C	ASN A 328	0	6.986	42.410	48.158	1.00	23.12
	ATOM	2499	O	ASN A 328	0	6.140	43.030	48.799	1.00	22.76

	ATOM	2500	CB	ASN A 328	0	8.223	41.603	50.121	1.00	23.09
	ATOM	2501	CG	ASN A 328	0	9.569	41.204	50.693	1.00	24.61
	ATOM	2502	OD1	ASN A 328	0	10.181	40.188	50.295	1.00	25.87
	ATOM	2503	ND2	ASN A 328	0	10.017	42.029	51.617	1.00	21.47
5	ATOM	2504	N	LEU A 329	0	6.776	42.000	46.923	1.00	23.14
	ATOM	2505	CA	LEU A 329	0	5.497	42.179	46.268	1.00	24.23
	ATOM	2506	C	LEU A 329	0	4.859	40.822	45.953	1.00	25.21
	ATOM	2507	O	LEU A 329	0	5.489	39.876	45.469	1.00	24.20
	ATOM	2508	CB	LEU A 329	0	5.622	42.963	44.948	1.00	24.33
10	ATOM	2509	CG	LEU A 329	0	6.369	44.279	45.082	1.00	26.30
	ATOM	2510	CD1	LEU A 329	0	6.778	44.884	43.757	1.00	26.24
	ATOM	2511	CD2	LEU A 329	0	5.550	45.249	45.913	1.00	27.07
	ATOM	2512	N	ARG A 330	0	3.562	40.806	46.204	1.00	25.13
	ATOM	2513	CA	ARG A 330	0	2.740	39.641	45.899	1.00	27.48
15	ATOM	2514	C	ARG A 330	0	1.628	40.116	44.965	1.00	27.52
	ATOM	2515	O	ARG A 330	0	0.988	41.132	45.257	1.00	27.17
	ATOM	2516	CB	ARG A 330	0	2.200	39.017	47.166	1.00	29.82
	ATOM	2517	CG	ARG A 330	0	1.351	37.794	46.932	1.00	33.18
	ATOM	2518	CD	ARG A 330	0	0.880	37.251	48.284	1.00	37.06
20	ATOM	2519	NE	ARG A 330	0	0.305	35.914	48.038	1.00	40.34
	ATOM	2520	CZ	ARG A 330	0	1.009	34.803	48.298	1.00	40.82
	ATOM	2521	NH1	ARG A 330	0	2.229	34.903	48.812	1.00	40.36
	ATOM	2522	NH2	ARG A 330	0	0.415	33.642	48.040	1.00	41.33
	ATOM	2523	N	PHE A 331	0	1.507	39.481	43.795	1.00	25.88
25	ATOM	2524	CA	PHE A 331	0	0.475	39.937	42.855	1.00	25.87
	ATOM	2525	C	PHE A 331	0	-0.657	38.919	42.779	1.00	25.94
	ATOM	2526	O	PHE A 331	0	-0.441	37.697	42.824	1.00	24.61
	ATOM	2527	CB	PHE A 331	0	1.102	40.269	41.511	1.00	25.94
	ATOM	2528	CG	PHE A 331	0	1.884	41.565	41.496	1.00	28.66
30	ATOM	2529	CD1	PHE A 331	0	1.282	42.782	41.759	1.00	28.04
	ATOM	2530	CD2	PHE A 331	0	3.246	41.569	41.214	1.00	29.71
	ATOM	2531	CE1	PHE A 331	0	1.988	43.963	41.744	1.00	29.21
	ATOM	2532	CE2	PHE A 331	0	3.975	42.753	41.181	1.00	30.61
	ATOM	2533	CZ	PHE A 331	0	3.348	43.965	41.453	1.00	30.66
35	ATOM	2534	N	GLN A 332	0	-1.873	39.446	42.676	1.00	25.58
	ATOM	2535	CA	GLN A 332	0	-3.085	38.628	42.608	1.00	26.60
	ATOM	2536	C	GLN A 332	0	-3.672	38.698	41.203	1.00	23.61
	ATOM	2537	O	GLN A 332	0	-4.136	39.739	40.755	1.00	21.73

ATOM 2538 CB GLN A 332 O -4.110 39.094 43.630 1.00 30.32
ATOM 2539 CG GLN A 332 O -5.412 38.299 43.642 1.00 35.72
ATOM 2540 CD GLN A 332 O -5.199 36.961 44.325 1.00 39.98
ATOM 2541 OE1 GLN A 332 O -5.859 35.961 44.007 1.00 42.32
5 ATOM 2542 NE2 GLN A 332 O -4.257 36.915 45.270 1.00 42.27
ATOM 2543 N LEU A 333 O -3.612 37.576 40.504 1.00 23.60
ATOM 2544 CA LEU A 333 O -4.105 37.565 39.118 1.00 26.25
ATOM 2545 C LEU A 333 O -5.627 37.373 39.123 1.00 26.55
ATOM 2546 O LEU A 333 O -6.107 36.655 39.998 1.00 25.70
10 ATOM 2547 CB LEU A 333 O -3.424 36.465 38.304 1.00 25.25
ATOM 2548 CG LEU A 333 O -1.919 36.608 38.052 1.00 25.72
ATOM 2549 CD1 LEU A 333 O -1.431 35.565 37.067 1.00 23.66
ATOM 2550 CD2 LEU A 333 O -1.551 38.000 37.558 1.00 25.25
ATOM 2551 N GLY A 334 O -6.327 37.976 38.188 1.00 27.85
15 ATOM 2552 CA GLY A 334 O -7.770 37.782 38.118 1.00 29.96
ATOM 2553 C GLY A 334 O -8.253 37.802 36.672 1.00 32.36
ATOM 2554 O GLY A 334 O -7.559 38.175 35.719 1.00 30.74
ATOM 2555 N PHE A 335 O -9.502 37.377 36.544 1.00 34.76
ATOM 2556 CA PHE A 335 O -10.181 37.360 35.260 1.00 38.54
20 ATOM 2557 C PHE A 335 O -11.625 37.806 35.514 1.00 41.05
ATOM 2558 O PHE A 335 O -12.443 37.028 36.021 1.00 41.53
ATOM 2559 CB PHE A 335 O -10.183 36.003 34.586 1.00 39.00
ATOM 2560 CG PHE A 335 O -10.772 36.105 33.197 1.00 40.61
ATOM 2561 CD1 PHE A 335 O -10.052 36.686 32.175 1.00 40.45
25 ATOM 2562 CD2 PHE A 335 O -12.045 35.614 32.942 1.00 41.39
ATOM 2563 CE1 PHE A 335 O -10.580 36.778 30.901 1.00 40.81
ATOM 2564 CE2 PHE A 335 O -12.588 35.697 31.671 1.00 41.51
ATOM 2565 CZ PHE A 335 O -11.849 36.281 30.652 1.00 41.87
ATOM 2566 N SER A 336 O -11.861 39.075 35.193 1.00 42.39
30 ATOM 2567 CA SER A 336 O -13.203 39.582 35.445 1.00 44.12
ATOM 2568 C SER A 336 O -13.704 40.525 34.370 1.00 44.31
ATOM 2569 O SER A 336 O -13.028 41.440 33.903 1.00 44.49
ATOM 2570 CB SER A 336 O -13.214 40.206 36.842 1.00 45.46
ATOM 2571 OG SER A 336 O -13.727 39.233 37.758 1.00 47.11
35 ATOM 2572 N GLY A 337 O -14.963 40.267 33.983 1.00 44.12
ATOM 2573 CA GLY A 337 O -15.630 41.067 32.959 1.00 41.89
ATOM 2574 C GLY A 337 O -14.963 40.920 31.608 1.00 40.08
ATOM 2575 O GLY A 337 O -14.712 41.891 30.888 1.00 41.35

ATOM 2576 N GLY A 338 0 -14.583 39.699 31.263 1.00 39.12
ATOM 2577 CA GLY A 338 0 -13.899 39.364 30.034 1.00 36.11
ATOM 2578 C GLY A 338 0 -12.503 39.970 29.929 1.00 34.97
ATOM 2579 O GLY A 338 0 -12.005 40.116 28.806 1.00 33.64
5 ATOM 2580 N ARG A 339 0 -11.885 40.355 31.048 1.00 33.21
ATOM 2581 CA ARG A 339 0 -10.538 40.916 30.982 1.00 32.04
ATOM 2582 C ARG A 339 0 -9.724 40.397 32.164 1.00 29.23
ATOM 2583 O ARG A 339 0 -10.260 40.053 33.210 1.00 26.38
ATOM 2584 CB ARG A 339 0 -10.495 42.419 30.845 1.00 36.52
10 ATOM 2585 CG ARG A 339 0 -11.291 43.281 31.790 1.00 42.08
ATOM 2586 CD ARG A 339 0 -11.895 44.502 31.127 1.00 45.03
ATOM 2587 NE ARG A 339 0 -11.046 45.380 30.351 1.00 47.77
ATOM 2588 CZ ARG A 339 0 -10.635 46.616 30.664 1.00 49.55
ATOM 2589 NH1 ARG A 339 0 -10.935 47.242 31.799 1.00 49.60
15 ATOM 2590 NH2 ARG A 339 0 -9.862 47.295 29.805 1.00 49.96
ATOM 2591 N PHE A 340 0 -8.425 40.181 31.900 1.00 25.50
ATOM 2592 CA PHE A 340 0 -7.526 39.713 32.938 1.00 22.68
ATOM 2593 C PHE A 340 0 -7.171 40.945 33.774 1.00 22.15
ATOM 2594 O PHE A 340 0 -7.069 42.069 33.266 1.00 21.26
20 ATOM 2595 CB PHE A 340 0 -6.210 39.135 32.397 1.00 22.39
ATOM 2596 CG PHE A 340 0 -6.333 37.792 31.736 1.00 20.74
ATOM 2597 CD1 PHE A 340 0 -6.338 37.710 30.357 1.00 20.97
ATOM 2598 CD2 PHE A 340 0 -6.448 36.644 32.468 1.00 21.19
ATOM 2599 CE1 PHE A 340 0 -6.449 36.488 29.721 1.00 21.61
25 ATOM 2600 CE2 PHE A 340 0 -6.585 35.408 31.826 1.00 22.99
ATOM 2601 CZ PHE A 340 0 -6.578 35.334 30.444 1.00 19.90
ATOM 2602 N THR A 341 0 -7.000 40.736 35.069 1.00 20.76
ATOM 2603 CA THR A 341 0 -6.605 41.879 35.889 1.00 21.55
ATOM 2604 C THR A 341 0 -5.400 41.509 36.759 1.00 21.00
30 ATOM 2605 O THR A 341 0 -5.236 40.329 37.089 1.00 20.70
ATOM 2606 CB THR A 341 0 -7.757 42.255 36.853 1.00 21.12
ATOM 2607 OG1 THR A 341 0 -8.014 41.102 37.668 1.00 21.26
ATOM 2608 CG2 THR A 341 0 -9.050 42.630 36.150 1.00 21.74
ATOM 2609 N ILE A 342 0 -4.750 42.529 37.308 1.00 20.28
35 ATOM 2610 CA ILE A 342 0 -3.739 42.273 38.333 1.00 20.34
ATOM 2611 C ILE A 342 0 -4.026 43.212 39.496 1.00 18.92
ATOM 2612 O ILE A 342 0 -4.004 44.437 39.327 1.00 16.42
ATOM 2613 CB ILE A 342 0 -2.306 42.439 37.820 1.00 21.04

	ATOM	2614	CG1	ILE	A	342	0	-1.337	42.721	38.988	1.00	21.39
	ATOM	2615	CG2	ILE	A	342	0	-2.250	43.540	36.800	1.00	24.57
	ATOM	2616	CD1	ILE	A	342	0	-0.260	41.661	38.949	1.00	24.53
	ATOM	2617	N	ASN	A	343	0	-4.282	42.601	40.650	1.00	17.77
5	ATOM	2618	CA	ASN	A	343	0	-4.702	43.413	41.782	1.00	21.51
	ATOM	2619	C	ASN	A	343	0	-5.881	44.287	41.394	1.00	21.43
	ATOM	2620	O	ASN	A	343	0	-5.903	45.495	41.598	1.00	20.26
	ATOM	2621	CB	ASN	A	343	0	-3.513	44.231	42.356	1.00	22.34
	ATOM	2622	CG	ASN	A	343	0	-2.685	43.190	43.073	1.00	25.38
10	ATOM	2623	OD1	ASN	A	343	0	-2.075	42.218	42.598	1.00	26.90
	ATOM	2624	ND2	ASN	A	343	0	-2.652	43.238	44.425	1.00	25.34
	ATOM	2625	N	GLY	A	344	0	-6.875	43.703	40.730	1.00	23.77
	ATOM	2626	CA	GLY	A	344	0	-8.078	44.406	40.324	1.00	25.28
	ATOM	2627	C	GLY	A	344	0	-7.954	45.280	39.111	1.00	26.82
15	ATOM	2628	O	GLY	A	344	0	-9.029	45.728	38.672	1.00	29.56
	ATOM	2629	N	THR	A	345	0	-6.798	45.561	38.527	1.00	26.28
	ATOM	2630	CA	THR	A	345	0	-6.766	46.440	37.366	1.00	25.48
	ATOM	2631	C	THR	A	345	0	-6.343	45.703	36.109	1.00	26.49
	ATOM	2632	O	THR	A	345	0	-5.385	44.925	36.122	1.00	28.22
20	ATOM	2633	CB	THR	A	345	0	-5.829	47.648	37.589	1.00	26.17
	ATOM	2634	OG1	THR	A	345	0	-6.191	48.334	38.788	1.00	25.32
	ATOM	2635	CG2	THR	A	345	0	-5.867	48.677	36.462	1.00	24.83
	ATOM	2636	N	ALA	A	346	0	-7.017	46.012	35.008	1.00	24.80
	ATOM	2637	CA	ALA	A	346	0	-6.768	45.491	33.688	1.00	23.82
25	ATOM	2638	C	ALA	A	346	0	-5.862	46.511	32.997	1.00	23.77
	ATOM	2639	O	ALA	A	346	0	-6.098	47.711	33.088	1.00	22.93
	ATOM	2640	CB	ALA	A	346	0	-8.031	45.353	32.841	1.00	24.13
	ATOM	2641	N	TYR	A	347	0	-4.793	46.023	32.392	1.00	22.69
	ATOM	2642	CA	TYR	A	347	0	-3.862	46.949	31.792	1.00	22.75
30	ATOM	2643	C	TYR	A	347	0	-4.483	47.532	30.527	1.00	23.42
	ATOM	2644	O	TYR	A	347	0	-4.954	46.753	29.709	1.00	22.19
	ATOM	2645	CB	TYR	A	347	0	-2.521	46.274	31.455	1.00	21.25
	ATOM	2646	CG	TYR	A	347	0	-1.584	47.221	30.732	1.00	18.93
	ATOM	2647	CD1	TYR	A	347	0	-0.819	48.137	31.442	1.00	18.17
35	ATOM	2648	CD2	TYR	A	347	0	-1.473	47.176	29.353	1.00	19.30
	ATOM	2649	CE1	TYR	A	347	0	0.034	49.003	30.763	1.00	18.37
	ATOM	2650	CE2	TYR	A	347	0	-0.650	48.063	28.664	1.00	18.40
	ATOM	2651	CZ	TYR	A	347	0	0.102	48.962	29.394	1.00	18.99

ATOM 2652 OH TYR A 347 0 0.947 49.802 28.706 1.00 19.65
ATOM 2653 N GLU A 348 0 -4.378 48.833 30.359 1.00 25.22
ATOM 2654 CA GLU A 348 0 -4.769 49.453 29.098 1.00 28.77
ATOM 2655 C GLU A 348 0 -3.659 50.470 28.805 1.00 27.38
5 ATOM 2656 O GLU A 348 0 -3.297 51.229 29.704 1.00 28.49
ATOM 2657 CB GLU A 348 0 -6.114 50.134 29.110 1.00 32.95
ATOM 2658 CG GLU A 348 0 -7.391 49.302 29.072 1.00 39.29
ATOM 2659 CD GLU A 348 0 -8.562 50.170 29.559 1.00 43.20
ATOM 2660 OE1 GLU A 348 0 -8.825 51.211 28.900 1.00 45.31
10 ATOM 2661 OE2 GLU A 348 0 -9.175 49.855 30.601 1.00 44.11
ATOM 2662 N SER A 349 0 -3.168 50.541 27.621 1.00 25.73
ATOM 2663 CA SER A 349 0 -2.080 51.410 27.201 1.00 28.25
ATOM 2664 C SER A 349 0 -2.401 52.887 27.194 1.00 28.71
ATOM 2665 O SER A 349 0 -3.279 53.399 26.526 1.00 29.13
15 ATOM 2666 CB SER A 349 0 -1.743 50.818 25.838 1.00 28.54
ATOM 2667 OG SER A 349 0 -0.850 51.499 25.026 1.00 33.31
ATOM 2668 N PRO A 350 0 -1.623 53.700 27.898 1.00 29.56
ATOM 2669 CA PRO A 350 0 -1.770 55.145 27.997 1.00 28.53
ATOM 2670 C PRO A 350 0 -1.480 55.825 26.679 1.00 28.01
20 ATOM 2671 O PRO A 350 0 -0.787 55.217 25.856 1.00 26.93
ATOM 2672 CB PRO A 350 0 -0.752 55.632 29.063 1.00 27.91
ATOM 2673 CG PRO A 350 0 0.309 54.560 28.863 1.00 28.03
ATOM 2674 CD PRO A 350 0 -0.461 53.245 28.688 1.00 28.76
ATOM 2675 N SER A 351 0 -1.951 57.066 26.485 1.00 28.89
25 ATOM 2676 CA SER A 351 0 -1.630 57.718 25.206 1.00 29.67
ATOM 2677 C SER A 351 0 -0.213 58.287 25.257 1.00 27.67
ATOM 2678 O SER A 351 0 0.320 58.524 24.177 1.00 28.18
ATOM 2679 CB SER A 351 0 -2.566 58.860 24.790 1.00 31.71
ATOM 2680 OG SER A 351 0 -2.793 59.679 25.938 1.00 34.19
30 ATOM 2681 N VAL A 352 0 0.316 58.529 26.449 1.00 25.32
ATOM 2682 CA VAL A 352 0 1.703 58.997 26.534 1.00 25.27
ATOM 2683 C VAL A 352 0 2.503 57.872 27.211 1.00 23.63
ATOM 2684 O VAL A 352 0 2.181 57.493 28.323 1.00 23.26
ATOM 2685 CB VAL A 352 0 1.934 60.300 27.303 1.00 24.91
35 ATOM 2686 CG1 VAL A 352 0 1.129 61.436 26.658 1.00 24.41
ATOM 2687 CG2 VAL A 352 0 3.424 60.635 27.281 1.00 23.35
ATOM 2688 N PRO A 353 0 3.498 57.375 26.510 1.00 22.39
ATOM 2689 CA PRO A 353 0 4.342 56.300 26.983 1.00 21.86

	ATOM	2690	C	PRO A 353	0	4.978	56.699	28.300	1.00	20.91
	ATOM	2691	O	PRO A 353	0	5.393	57.852	28.483	1.00	21.91
	ATOM	2692	CB	PRO A 353	0	5.417	56.054	25.916	1.00	23.95
	ATOM	2693	CG	PRO A 353	0	5.181	57.123	24.878	1.00	23.79
5	ATOM	2694	CD	PRO A 353	0	3.882	57.848	25.180	1.00	23.03
	ATOM	2695	N	THR A 354	0	5.043	55.778	29.234	1.00	18.66
	ATOM	2696	CA	THR A 354	0	5.646	56.015	30.530	1.00	18.05
	ATOM	2697	C	THR A 354	0	6.981	56.739	30.478	1.00	18.33
	ATOM	2698	O	THR A 354	0	7.168	57.630	31.319	1.00	19.46
10	ATOM	2699	CB	THR A 354	0	5.871	54.661	31.242	1.00	17.10
	ATOM	2700	OG1	THR A 354	0	4.903	53.710	30.797	1.00	17.24
	ATOM	2701	CG2	THR A 354	0	5.772	54.852	32.741	1.00	16.43
	ATOM	2702	N	LEU A 355	0	7.940	56.380	29.618	1.00	17.49
	ATOM	2703	CA	LEU A 355	0	9.215	57.076	29.604	1.00	18.84
15	ATOM	2704	C	LEU A 355	0	9.013	58.579	29.284	1.00	19.80
	ATOM	2705	O	LEU A 355	0	9.722	59.417	29.849	1.00	17.13
	ATOM	2706	CB	LEU A 355	0	10.200	56.498	28.622	1.00	17.89
	ATOM	2707	CG	LEU A 355	0	11.703	56.488	28.819	1.00	18.66
	ATOM	2708	CD1	LEU A 355	0	12.436	56.851	27.547	1.00	18.37
20	ATOM	2709	CD2	LEU A 355	0	12.199	57.204	30.056	1.00	16.79
	ATOM	2710	N	LEU A 356	0	8.134	58.883	28.328	1.00	20.48
	ATOM	2711	CA	LEU A 356	0	7.812	60.274	27.993	1.00	21.62
	ATOM	2712	C	LEU A 356	0	7.085	60.932	29.163	1.00	21.28
	ATOM	2713	O	LEU A 356	0	7.497	62.042	29.506	1.00	22.01
25	ATOM	2714	CB	LEU A 356	0	7.028	60.474	26.700	1.00	22.08
	ATOM	2715	CG	LEU A 356	0	6.850	61.939	26.239	1.00	23.98
	ATOM	2716	CD1	LEU A 356	0	8.157	62.709	26.207	1.00	23.11
	ATOM	2717	CD2	LEU A 356	0	6.191	61.985	24.864	1.00	24.74
	ATOM	2718	N	GLN A 357	0	6.219	60.267	29.922	1.00	21.37
30	ATOM	2719	CA	GLN A 357	0	5.669	60.893	31.120	1.00	21.87
	ATOM	2720	C	GLN A 357	0	6.759	61.254	32.128	1.00	24.12
	ATOM	2721	O	GLN A 357	0	6.674	62.277	32.811	1.00	24.92
	ATOM	2722	CB	GLN A 357	0	4.636	60.015	31.822	1.00	20.63
	ATOM	2723	CG	GLN A 357	0	3.447	59.674	30.906	1.00	19.17
35	ATOM	2724	CD	GLN A 357	0	2.547	58.643	31.540	1.00	18.85
	ATOM	2725	OE1	GLN A 357	0	2.162	58.748	32.713	1.00	19.06
	ATOM	2726	NE2	GLN A 357	0	2.262	57.600	30.742	1.00	18.49
	ATOM	2727	N	ILE A 358	0	7.735	60.371	32.346	1.00	25.66

	ATOM	2728	CA	ILE A 358	0	8.822	60.651	33.263	1.00	26.19
	ATOM	2729	C	ILE A 358	0	9.699	61.800	32.762	1.00	27.66
	ATOM	2730	O	ILE A 358	0	9.940	62.725	33.551	1.00	26.65
	ATOM	2731	CB	ILE A 358	0	9.692	59.420	33.578	1.00	24.79
5	ATOM	2732	CG1	ILE A 358	0	8.807	58.395	34.304	1.00	24.09
	ATOM	2733	CG2	ILE A 358	0	10.865	59.841	34.451	1.00	23.78
	ATOM	2734	CD1	ILE A 358	0	9.251	56.954	34.234	1.00	23.34
	ATOM	2735	N	MET A 359	0	10.054	61.844	31.486	1.00	29.63
	ATOM	2736	CA	MET A 359	0	10.893	62.910	30.965	1.00	33.02
10	ATOM	2737	C	MET A 359	0	10.174	64.260	31.027	1.00	34.46
	ATOM	2738	O	MET A 359	0	10.801	65.324	31.026	1.00	33.77
	ATOM	2739	CB	MET A 359	0	11.346	62.664	29.537	1.00	35.67
	ATOM	2740	CG	MET A 359	0	12.065	61.403	29.138	1.00	40.75
	ATOM	2741	SD	MET A 359	0	13.764	61.153	29.671	1.00	44.90
15	ATOM	2742	CE	MET A 359	0	14.594	62.592	29.007	1.00	44.24
	ATOM	2743	N	SER A 360	0	8.835	64.238	31.070	1.00	33.43
	ATOM	2744	CA	SER A 360	0	8.024	65.430	31.088	1.00	32.92
	ATOM	2745	C	SER A 360	0	7.761	65.995	32.474	1.00	33.24
	ATOM	2746	O	SER A 360	0	6.989	66.966	32.556	1.00	34.08
20	ATOM	2747	CB	SER A 360	0	6.678	65.134	30.393	1.00	31.34
	ATOM	2748	OG	SER A 360	0	6.928	65.109	28.996	1.00	31.06
	ATOM	2749	N	GLY A 361	0	8.288	65.360	33.517	1.00	32.06
	ATOM	2750	CA	GLY A 361	0	8.072	65.868	34.847	1.00	31.80
	ATOM	2751	C	GLY A 361	0	7.487	64.955	35.880	1.00	32.48
25	ATOM	2752	O	GLY A 361	0	7.420	65.377	37.043	1.00	33.20
	ATOM	2753	N	ALA A 362	0	6.991	63.769	35.535	1.00	33.69
	ATOM	2754	CA	ALA A 362	0	6.406	62.926	36.601	1.00	35.10
	ATOM	2755	C	ALA A 362	0	7.475	62.615	37.650	1.00	34.45
	ATOM	2756	O	ALA A 362	0	8.598	62.306	37.286	1.00	33.60
30	ATOM	2757	CB	ALA A 362	0	5.789	61.658	36.043	1.00	34.88
	ATOM	2758	N	GLN A 363	0	7.146	62.676	38.920	1.00	36.22
	ATOM	2759	CA	GLN A 363	0	8.083	62.458	40.007	1.00	37.87
	ATOM	2760	C	GLN A 363	0	7.776	61.189	40.787	1.00	37.20
	ATOM	2761	O	GLN A 363	0	8.620	60.777	41.587	1.00	36.79
35	ATOM	2762	CB	GLN A 363	0	8.012	63.619	41.022	1.00	40.41
	ATOM	2763	CG	GLN A 363	0	8.986	64.740	40.721	1.00	44.07
	ATOM	2764	CD	GLN A 363	0	8.586	66.154	41.092	1.00	45.77
	ATOM	2765	OE1	GLN A 363	0	7.697	66.473	41.901	1.00	46.53

	ATOM	2766	NE2	GLN	A	363	0	9.294	67.089	40.435	1.00	46.12
	ATOM	2767	N	SER	A	364	0	6.579	60.632	40.610	1.00	35.74
	ATOM	2768	CA	SER	A	364	0	6.249	59.434	41.381	1.00	34.54
	ATOM	2769	C	SER	A	364	0	5.225	58.588	40.653	1.00	34.32
5	ATOM	2770	O	SER	A	364	0	4.605	59.037	39.692	1.00	33.71
	ATOM	2771	CB	SER	A	364	0	5.774	59.835	42.769	1.00	35.68
	ATOM	2772	OG	SER	A	364	0	4.396	60.095	42.928	1.00	35.86
	ATOM	2773	N	ALA	A	365	0	5.015	57.372	41.146	1.00	33.95
	ATOM	2774	CA	ALA	A	365	0	4.017	56.486	40.564	1.00	34.62
10	ATOM	2775	C	ALA	A	365	0	2.637	57.148	40.560	1.00	34.46
	ATOM	2776	O	ALA	A	365	0	1.906	56.995	39.582	1.00	34.37
	ATOM	2777	CB	ALA	A	365	0	3.963	55.155	41.301	1.00	33.51
	ATOM	2778	N	ASN	A	366	0	2.261	57.916	41.571	1.00	34.45
	ATOM	2779	CA	ASN	A	366	0	1.003	58.619	41.632	1.00	36.37
15	ATOM	2780	C	ASN	A	366	0	0.708	59.524	40.447	1.00	35.60
	ATOM	2781	O	ASN	A	366	0	-0.462	59.719	40.131	1.00	36.50
	ATOM	2782	CB	ASN	A	366	0	0.904	59.464	42.918	1.00	38.72
	ATOM	2783	CG	ASN	A	366	0	0.794	58.558	44.126	1.00	41.08
	ATOM	2784	OD1	ASN	A	366	0	0.863	58.966	45.284	1.00	43.39
20	ATOM	2785	ND2	ASN	A	366	0	0.646	57.256	43.914	1.00	42.72
	ATOM	2786	N	ASP	A	367	0	1.694	60.046	39.752	1.00	34.06
	ATOM	2787	CA	ASP	A	367	0	1.571	60.899	38.610	1.00	33.37
	ATOM	2788	C	ASP	A	367	0	1.566	60.122	37.293	1.00	32.09
	ATOM	2789	O	ASP	A	367	0	1.430	60.762	36.247	1.00	31.74
25	ATOM	2790	CB	ASP	A	367	0	2.768	61.841	38.483	1.00	35.96
	ATOM	2791	CG	ASP	A	367	0	3.048	62.818	39.602	1.00	37.69
	ATOM	2792	OD1	ASP	A	367	0	2.123	63.209	40.336	1.00	37.23
	ATOM	2793	OD2	ASP	A	367	0	4.258	63.194	39.705	1.00	39.62
	ATOM	2794	N	LEU	A	368	0	1.791	58.814	37.371	1.00	30.39
30	ATOM	2795	CA	LEU	A	368	0	1.897	58.055	36.123	1.00	28.74
	ATOM	2796	C	LEU	A	368	0	0.586	57.386	35.745	1.00	28.85
	ATOM	2797	O	LEU	A	368	0	-0.214	56.947	36.555	1.00	28.17
	ATOM	2798	CB	LEU	A	368	0	3.043	57.046	36.194	1.00	26.94
	ATOM	2799	CG	LEU	A	368	0	4.436	57.668	36.422	1.00	27.05
35	ATOM	2800	CD1	LEU	A	368	0	5.455	56.581	36.765	1.00	25.41
	ATOM	2801	CD2	LEU	A	368	0	4.882	58.499	35.236	1.00	24.44
	ATOM	2802	N	LEU	A	369	0	0.392	57.332	34.446	1.00	28.81
	ATOM	2803	CA	LEU	A	369	0	-0.753	56.671	33.834	1.00	29.65

	ATOM	2804	C	LEU A 369	0	-0.238	55.398	33.162	1.00	28.29
	ATOM	2805	O	LEU A 369	0	0.875	55.356	32.660	1.00	25.59
	ATOM	2806	CB	LEU A 369	0	-1.333	57.668	32.821	1.00	30.27
	ATOM	2807	CG	LEU A 369	0	-1.800	58.998	33.456	1.00	32.06
5	ATOM	2808	CD1	LEU A 369	0	-2.220	59.979	32.370	1.00	31.87
	ATOM	2809	CD2	LEU A 369	0	-2.932	58.787	34.455	1.00	30.89
	ATOM	2810	N	PRO A 370	0	-1.054	54.361	33.157	1.00	27.87
	ATOM	2811	CA	PRO A 370	0	-2.396	54.379	33.688	1.00	26.71
	ATOM	2812	C	PRO A 370	0	-2.513	54.112	35.169	1.00	26.73
10	ATOM	2813	O	PRO A 370	0	-1.872	53.184	35.668	1.00	26.55
	ATOM	2814	CB	PRO A 370	0	-3.126	53.222	32.958	1.00	27.28
	ATOM	2815	CG	PRO A 370	0	-2.003	52.317	32.557	1.00	27.38
	ATOM	2816	CD	PRO A 370	0	-0.720	53.102	32.482	1.00	27.24
	ATOM	2817	N	ALA A 371	0	-3.414	54.810	35.870	1.00	26.16
15	ATOM	2818	CA	ALA A 371	0	-3.581	54.556	37.302	1.00	25.73
	ATOM	2819	C	ALA A 371	0	-3.892	53.103	37.616	1.00	24.59
	ATOM	2820	O	ALA A 371	0	-4.758	52.533	36.946	1.00	25.05
	ATOM	2821	CB	ALA A 371	0	-4.718	55.394	37.903	1.00	26.42
	ATOM	2822	N	GLY A 372	0	-3.261	52.524	38.625	1.00	22.47
20	ATOM	2823	CA	GLY A 372	0	-3.519	51.187	39.087	1.00	21.06
	ATOM	2824	C	GLY A 372	0	-2.691	50.096	38.427	1.00	23.01
	ATOM	2825	O	GLY A 372	0	-2.758	48.928	38.831	1.00	23.85
	ATOM	2826	N	SER A 373	0	-1.910	50.428	37.421	1.00	23.30
	ATOM	2827	CA	SER A 373	0	-1.054	49.459	36.736	1.00	24.36
25	ATOM	2828	C	SER A 373	0	0.429	49.746	36.919	1.00	24.76
	ATOM	2829	O	SER A 373	0	1.257	49.103	36.270	1.00	25.75
	ATOM	2830	CB	SER A 373	0	-1.371	49.584	35.233	1.00	23.25
	ATOM	2831	OG	SER A 373	0	-2.638	49.014	34.952	1.00	23.80
	ATOM	2832	N	VAL A 374	0	0.779	50.799	37.657	1.00	23.87
30	ATOM	2833	CA	VAL A 374	0	2.176	51.255	37.706	1.00	22.95
	ATOM	2834	C	VAL A 374	0	2.739	51.109	39.105	1.00	21.72
	ATOM	2835	O	VAL A 374	0	2.093	51.518	40.059	1.00	21.03
	ATOM	2836	CB	VAL A 374	0	2.317	52.687	37.169	1.00	23.05
	ATOM	2837	CG1	VAL A 374	0	3.720	53.273	37.323	1.00	24.13
35	ATOM	2838	CG2	VAL A 374	0	1.945	52.771	35.698	1.00	21.58
	ATOM	2839	N	TYR A 375	0	3.862	50.402	39.246	1.00	20.52
	ATOM	2840	CA	TYR A 375	0	4.445	50.184	40.573	1.00	22.02
	ATOM	2841	C	TYR A 375	0	5.873	50.743	40.549	1.00	22.56

	ATOM	2842	O	TYR A 375	0	6.665	50.524	39.639	1.00	21.82
	ATOM	2843	CB	TYR A 375	0	4.467	48.729	41.067	1.00	21.98
	ATOM	2844	CG	TYR A 375	0	3.042	48.217	41.226	1.00	24.04
	ATOM	2845	CD1	TYR A 375	0	2.398	48.261	42.445	1.00	23.57
5	ATOM	2846	CD2	TYR A 375	0	2.339	47.760	40.115	1.00	24.92
	ATOM	2847	CE1	TYR A 375	0	1.100	47.831	42.575	1.00	25.65
	ATOM	2848	CE2	TYR A 375	0	1.034	47.327	40.220	1.00	25.89
	ATOM	2849	CZ	TYR A 375	0	0.429	47.352	41.464	1.00	26.65
	ATOM	2850	OH	TYR A 375	0	-0.869	46.916	41.593	1.00	27.26
10	ATOM	2851	N	GLU A 376	0	6.130	51.563	41.546	1.00	22.36
	ATOM	2852	CA	GLU A 376	0	7.403	52.214	41.718	1.00	23.62
	ATOM	2853	C	GLU A 376	0	8.411	51.289	42.387	1.00	22.40
	ATOM	2854	O	GLU A 376	0	8.062	50.578	43.324	1.00	21.88
	ATOM	2855	CB	GLU A 376	0	7.211	53.465	42.614	1.00	25.13
15	ATOM	2856	CG	GLU A 376	0	8.500	54.255	42.720	1.00	27.91
	ATOM	2857	CD	GLU A 376	0	8.376	55.725	43.046	1.00	29.20
	ATOM	2858	OE1	GLU A 376	0	7.247	56.268	43.109	1.00	30.01
	ATOM	2859	OE2	GLU A 376	0	9.458	56.336	43.219	1.00	28.05
	ATOM	2860	N	LEU A 377	0	9.669	51.353	41.954	1.00	21.23
20	ATOM	2861	CA	LEU A 377	0	10.705	50.535	42.626	1.00	19.95
	ATOM	2862	C	LEU A 377	0	11.838	51.478	42.982	1.00	20.30
	ATOM	2863	O	LEU A 377	0	12.220	52.350	42.197	1.00	20.12
	ATOM	2864	CB	LEU A 377	0	11.129	49.419	41.692	1.00	20.77
	ATOM	2865	CG	LEU A 377	0	10.668	47.964	41.818	1.00	20.49
25	ATOM	2866	CD1	LEU A 377	0	9.439	47.739	42.629	1.00	17.77
	ATOM	2867	CD2	LEU A 377	0	10.617	47.242	40.483	1.00	19.28
	ATOM	2868	N	PRO A 378	0	12.407	51.334	44.162	1.00	19.69
	ATOM	2869	CA	PRO A 378	0	13.523	52.117	44.631	1.00	19.91
	ATOM	2870	C	PRO A 378	0	14.797	51.650	43.937	1.00	19.81
30	ATOM	2871	O	PRO A 378	0	14.795	50.645	43.241	1.00	17.74
	ATOM	2872	CB	PRO A 378	0	13.611	51.893	46.157	1.00	20.21
	ATOM	2873	CG	PRO A 378	0	12.957	50.546	46.291	1.00	20.73
	ATOM	2874	CD	PRO A 378	0	12.050	50.292	45.114	1.00	19.74
	ATOM	2875	N	ARG A 379	0	15.877	52.410	44.059	1.00	19.68
35	ATOM	2876	CA	ARG A 379	0	17.172	52.135	43.449	1.00	18.58
	ATOM	2877	C	ARG A 379	0	18.027	51.129	44.193	1.00	18.68
	ATOM	2878	O	ARG A 379	0	18.151	51.126	45.432	1.00	17.60
	ATOM	2879	CB	ARG A 379	0	17.946	53.487	43.431	1.00	18.33

	ATOM	2880	CG	ARG A 379	0	19.406	53.348	43.030	1.00	19.33
	ATOM	2881	CD	ARG A 379	0	20.026	54.710	42.729	1.00	19.06
	ATOM	2882	NE	ARG A 379	0	21.413	54.561	42.295	1.00	16.65
	ATOM	2883	CZ	ARG A 379	0	21.794	54.681	41.031	1.00	15.60
5	ATOM	2884	NH1	ARG A 379	0	20.964	54.904	40.038	1.00	14.29
	ATOM	2885	NH2	ARG A 379	0	23.096	54.505	40.783	1.00	17.29
	ATOM	2886	N	ASN A 380	0	18.701	50.263	43.441	1.00	20.11
	ATOM	2887	CA	ASN A 380	0	19.658	49.328	44.011	1.00	21.97
	ATOM	2888	C	ASN A 380	0	19.129	48.604	45.227	1.00	22.44
10	ATOM	2889	O	ASN A 380	0	19.712	48.630	46.317	1.00	22.53
	ATOM	2890	CB	ASN A 380	0	20.995	50.045	44.345	1.00	23.30
	ATOM	2891	CG	ASN A 380	0	21.860	50.231	43.107	1.00	25.83
	ATOM	2892	OD1	ASN A 380	0	22.636	51.186	42.877	1.00	27.14
	ATOM	2893	ND2	ASN A 380	0	21.767	49.271	42.185	1.00	24.91
15	ATOM	2894	N	GLN A 381	0	17.974	47.936	45.097	1.00	21.39
	ATOM	2895	CA	GLN A 381	0	17.468	47.162	46.220	1.00	20.88
	ATOM	2896	C	GLN A 381	0	17.169	45.760	45.679	1.00	19.96
	ATOM	2897	O	GLN A 381	0	17.000	45.635	44.471	1.00	19.90
	ATOM	2898	CB	GLN A 381	0	16.219	47.722	46.871	1.00	22.84
20	ATOM	2899	CG	GLN A 381	0	16.326	49.172	47.318	1.00	27.28
	ATOM	2900	CD	GLN A 381	0	16.065	49.297	48.792	1.00	30.24
	ATOM	2901	OE1	GLN A 381	0	15.067	49.917	49.171	1.00	34.48
	ATOM	2902	NE2	GLN A 381	0	16.929	48.742	49.611	1.00	30.80
	ATOM	2903	N	VAL A 382	0	17.046	44.825	46.594	1.00	18.67
25	ATOM	2904	CA	VAL A 382	0	16.665	43.472	46.248	1.00	18.98
	ATOM	2905	C	VAL A 382	0	15.139	43.327	46.212	1.00	19.75
	ATOM	2906	O	VAL A 382	0	14.443	43.550	47.225	1.00	18.76
	ATOM	2907	CB	VAL A 382	0	17.252	42.491	47.278	1.00	19.03
	ATOM	2908	CG1	VAL A 382	0	16.811	41.065	46.960	1.00	18.87
30	ATOM	2909	CG2	VAL A 382	0	18.779	42.637	47.344	1.00	17.54
	ATOM	2910	N	VAL A 383	0	14.601	42.954	45.046	1.00	17.58
	ATOM	2911	CA	VAL A 383	0	13.151	42.715	45.037	1.00	17.76
	ATOM	2912	C	VAL A 383	0	12.777	41.254	44.883	1.00	17.50
	ATOM	2913	O	VAL A 383	0	13.348	40.472	44.153	1.00	16.42
35	ATOM	2914	CB	VAL A 383	0	12.306	43.626	44.145	1.00	17.69
	ATOM	2915	CG1	VAL A 383	0	13.111	44.759	43.585	1.00	15.33
	ATOM	2916	CG2	VAL A 383	0	11.400	43.009	43.126	1.00	17.79
	ATOM	2917	N	GLU A 384	0	11.743	40.861	45.638	1.00	18.47

	ATOM	2918	CA	GLU A 384	0	11.173	39.529	45.542	1.00	18.27
	ATOM	2919	C	GLU A 384	0	9.711	39.683	45.096	1.00	18.94
	ATOM	2920	O	GLU A 384	0	8.956	40.311	45.816	1.00	19.06
	ATOM	2921	CB	GLU A 384	0	11.253	38.764	46.852	1.00	17.12
5	ATOM	2922	CG	GLU A 384	0	10.717	37.345	46.738	1.00	17.52
	ATOM	2923	CD	GLU A 384	0	10.979	36.551	47.998	1.00	19.10
	ATOM	2924	OE1	GLU A 384	0	12.101	36.050	48.218	1.00	20.69
	ATOM	2925	OE2	GLU A 384	0	10.018	36.405	48.773	1.00	21.22
	ATOM	2926	N	LEU A 385	0	9.326	39.182	43.948	1.00	19.78
10	ATOM	2927	CA	LEU A 385	0	7.966	39.153	43.463	1.00	21.07
	ATOM	2928	C	LEU A 385	0	7.391	37.738	43.591	1.00	20.91
	ATOM	2929	O	LEU A 385	0	8.043	36.790	43.113	1.00	21.40
	ATOM	2930	CB	LEU A 385	0	7.881	39.466	41.959	1.00	20.92
	ATOM	2931	CG	LEU A 385	0	8.393	40.795	41.457	1.00	23.75
15	ATOM	2932	CD1	LEU A 385	0	8.118	40.984	39.962	1.00	23.01
	ATOM	2933	CD2	LEU A 385	0	7.827	41.977	42.244	1.00	22.40
	ATOM	2934	N	VAL A 386	0	6.182	37.574	44.099	1.00	20.91
	ATOM	2935	CA	VAL A 386	0	5.510	36.274	44.189	1.00	19.03
	ATOM	2936	C	VAL A 386	0	4.228	36.334	43.356	1.00	21.11
20	ATOM	2937	O	VAL A 386	0	3.465	37.326	43.516	1.00	20.56
	ATOM	2938	CB	VAL A 386	0	5.159	35.967	45.654	1.00	20.91
	ATOM	2939	CG1	VAL A 386	0	4.518	34.575	45.739	1.00	20.40
	ATOM	2940	CG2	VAL A 386	0	6.321	36.044	46.625	1.00	19.89
	ATOM	2941	N	VAL A 387	0	4.011	35.469	42.358	1.00	20.02
25	ATOM	2942	CA	VAL A 387	0	2.817	35.515	41.491	1.00	20.83
	ATOM	2943	C	VAL A 387	0	2.119	34.152	41.385	1.00	21.15
	ATOM	2944	O	VAL A 387	0	2.369	33.285	40.528	1.00	19.97
	ATOM	2945	CB	VAL A 387	0	3.163	36.076	40.104	1.00	20.91
	ATOM	2946	CG1	VAL A 387	0	1.917	36.472	39.297	1.00	22.49
30	ATOM	2947	CG2	VAL A 387	0	3.959	37.393	40.171	1.00	22.24
	ATOM	2948	N	PRO A 388	0	1.262	33.832	42.358	1.00	20.55
	ATOM	2949	CA	PRO A 388	0	0.570	32.548	42.483	1.00	20.93
	ATOM	2950	C	PRO A 388	0	-0.271	32.226	41.264	1.00	20.76
	ATOM	2951	O	PRO A 388	0	-0.928	33.118	40.715	1.00	19.53
35	ATOM	2952	CB	PRO A 388	0	-0.310	32.559	43.757	1.00	20.54
	ATOM	2953	CG	PRO A 388	0	0.280	33.766	44.482	1.00	21.86
	ATOM	2954	CD	PRO A 388	0	0.841	34.707	43.438	1.00	20.83
	ATOM	2955	N	ALA A 389	0	-0.160	30.986	40.807	1.00	21.68

ATOM 2956 CA ALA A 389 0 -0.983 30.617 39.640 1.00 24.20
ATOM 2957 C ALA A 389 0 -2.394 30.320 40.148 1.00 25.02
ATOM 2958 O ALA A 389 0 -2.619 30.162 41.350 1.00 24.19
ATOM 2959 CB ALA A 389 0 -0.383 29.403 38.968 1.00 23.67
5 ATOM 2960 N GLY A 390 0 -3.309 30.143 39.222 1.00 28.43
ATOM 2961 CA GLY A 390 0 -4.713 29.811 39.539 1.00 28.47
ATOM 2962 C GLY A 390 0 -5.624 30.325 38.431 1.00 28.63
ATOM 2963 O GLY A 390 0 -6.512 29.630 37.937 1.00 31.26
ATOM 2964 N VAL A 391 0 -5.402 31.531 37.961 1.00 27.11
10 ATOM 2965 CA VAL A 391 0 -6.234 32.164 36.962 1.00 26.51
ATOM 2966 C VAL A 391 0 -6.246 31.377 35.666 1.00 29.59
ATOM 2967 O VAL A 391 0 -5.274 30.775 35.181 1.00 30.61
ATOM 2968 CB VAL A 391 0 -5.835 33.634 36.788 1.00 25.83
ATOM 2969 CG1 VAL A 391 0 -4.584 33.787 35.937 1.00 24.18
15 ATOM 2970 CG2 VAL A 391 0 -7.017 34.419 36.219 1.00 24.11
ATOM 2971 N LEU A 392 0 -7.439 31.392 35.058 1.00 30.83
ATOM 2972 CA LEU A 392 0 -7.705 30.604 33.867 1.00 30.29
ATOM 2973 C LEU A 392 0 -6.809 31.004 32.710 1.00 27.38
ATOM 2974 O LEU A 392 0 -6.316 32.113 32.665 1.00 24.62
20 ATOM 2975 CB LEU A 392 0 -9.173 30.726 33.436 1.00 32.58
ATOM 2976 CG LEU A 392 0 -9.711 32.126 33.189 1.00 33.97
ATOM 2977 CD1 LEU A 392 0 -9.411 32.626 31.786 1.00 34.78
ATOM 2978 CD2 LEU A 392 0 -11.225 32.122 33.463 1.00 36.03
ATOM 2979 N GLY A 393 0 -6.725 30.074 31.754 1.00 26.24
25 ATOM 2980 CA GLY A 393 0 -5.936 30.302 30.554 1.00 25.54
ATOM 2981 C GLY A 393 0 -4.458 29.994 30.710 1.00 25.81
ATOM 2982 O GLY A 393 0 -3.686 30.361 29.820 1.00 26.67
ATOM 2983 N GLY A 394 0 -4.033 29.379 31.803 1.00 25.84
ATOM 2984 CA GLY A 394 0 -2.615 29.112 32.035 1.00 25.94
30 ATOM 2985 C GLY A 394 0 -2.140 27.844 31.348 1.00 26.00
ATOM 2986 O GLY A 394 0 -2.884 27.193 30.625 1.00 25.18
ATOM 2987 N PRO A 395 0 -0.860 27.527 31.517 1.00 24.26
ATOM 2988 CA PRO A 395 0 0.051 28.258 32.364 1.00 21.79
ATOM 2989 C PRO A 395 0 0.517 29.518 31.660 1.00 19.29
35 ATOM 2990 O PRO A 395 0 0.704 29.597 30.445 1.00 17.41
ATOM 2991 CB PRO A 395 0 1.159 27.279 32.794 1.00 22.52
ATOM 2992 CG PRO A 395 0 1.062 26.223 31.758 1.00 24.35
ATOM 2993 CD PRO A 395 0 -0.241 26.312 30.973 1.00 24.87

	ATOM	2994	N	HIS A 396	0	0.586	30.591	32.451	1.00	16.97
	ATOM	2995	CA	HIS A 396	0	0.970	31.917	31.980	1.00	15.05
	ATOM	2996	C	HIS A 396	0	2.477	32.137	32.186	1.00	15.41
	ATOM	2997	O	HIS A 396	0	3.039	32.025	33.275	1.00	14.21
5	ATOM	2998	CB	HIS A 396	0	0.288	32.989	32.842	1.00	15.40
	ATOM	2999	CG	HIS A 396	0	-1.224	32.924	32.737	1.00	18.23
	ATOM	3000	ND1	HIS A 396	0	-1.942	33.504	31.702	1.00	16.23
	ATOM	3001	CD2	HIS A 396	0	-2.109	32.319	33.557	1.00	17.00
	ATOM	3002	CE1	HIS A 396	0	-3.218	33.262	31.906	1.00	18.22
10	ATOM	3003	NE2	HIS A 396	0	-3.343	32.526	33.014	1.00	19.08
	ATOM	3004	N	PRO A 397	0	3.143	32.403	31.090	1.00	14.69
	ATOM	3005	CA	PRO A 397	0	4.593	32.617	31.080	1.00	16.91
	ATOM	3006	C	PRO A 397	0	4.818	34.129	31.202	1.00	17.59
	ATOM	3007	O	PRO A 397	0	4.524	34.843	30.235	1.00	17.59
15	ATOM	3008	CB	PRO A 397	0	5.076	32.040	29.757	1.00	16.63
	ATOM	3009	CG	PRO A 397	0	3.785	31.844	28.978	1.00	17.83
	ATOM	3010	CD	PRO A 397	0	2.620	32.464	29.736	1.00	14.36
	ATOM	3011	N	PHE A 398	0	5.242	34.590	32.377	1.00	16.39
	ATOM	3012	CA	PHE A 398	0	5.462	36.019	32.529	1.00	15.95
20	ATOM	3013	C	PHE A 398	0	6.906	36.365	32.168	1.00	15.74
	ATOM	3014	O	PHE A 398	0	7.846	35.619	32.444	1.00	15.78
	ATOM	3015	CB	PHE A 398	0	5.173	36.455	33.963	1.00	17.20
	ATOM	3016	CG	PHE A 398	0	3.817	37.073	34.169	1.00	19.23
	ATOM	3017	CD1	PHE A 398	0	2.673	36.299	34.005	1.00	19.58
25	ATOM	3018	CD2	PHE A 398	0	3.688	38.403	34.537	1.00	19.42
	ATOM	3019	CE1	PHE A 398	0	1.409	36.832	34.198	1.00	19.83
	ATOM	3020	CE2	PHE A 398	0	2.405	38.933	34.709	1.00	21.46
	ATOM	3021	CZ	PHE A 398	0	1.260	38.162	34.539	1.00	19.65
	ATOM	3022	N	HIS A 399	0	7.080	37.562	31.640	1.00	14.77
30	ATOM	3023	CA	HIS A 399	0	8.374	38.089	31.333	1.00	14.75
	ATOM	3024	C	HIS A 399	0	8.580	39.496	31.872	1.00	17.67
	ATOM	3025	O	HIS A 399	0	7.635	40.308	31.925	1.00	18.29
	ATOM	3026	CB	HIS A 399	0	8.582	37.968	29.861	1.00	14.01
	ATOM	3027	CG	HIS A 399	0	8.747	39.105	28.962	1.00	16.26
35	ATOM	3028	ND1	HIS A 399	0	9.957	39.511	28.446	1.00	15.35
	ATOM	3029	CD2	HIS A 399	0	7.788	39.903	28.386	1.00	17.58
	ATOM	3030	CE1	HIS A 399	0	9.764	40.507	27.593	1.00	15.61
	ATOM	3031	NE2	HIS A 399	0	8.457	40.770	27.548	1.00	17.52

ATOM 3032 N LEU A 400 0 9.837 39.771 32.201 1.00 15.57
ATOM 3033 CA LEU A 400 0 10.220 41.061 32.745 1.00 16.93
ATOM 3034 C LEU A 400 0 11.207 41.732 31.788 1.00 16.51
ATOM 3035 O LEU A 400 0 12.268 41.175 31.510 1.00 15.77
5 ATOM 3036 CB LEU A 400 0 10.913 40.825 34.084 1.00 18.17
ATOM 3037 CG LEU A 400 0 10.877 41.741 35.288 1.00 21.27
ATOM 3038 CD1 LEU A 400 0 12.130 41.638 36.151 1.00 19.27
ATOM 3039 CD2 LEU A 400 0 10.536 43.166 34.926 1.00 19.86
ATOM 3040 N HIS A 401 0 10.945 42.916 31.321 1.00 14.34
10 ATOM 3041 CA HIS A 401 0 11.830 43.707 30.508 1.00 16.06
ATOM 3042 C HIS A 401 0 12.924 44.300 31.428 1.00 16.15
ATOM 3043 O HIS A 401 0 12.644 44.543 32.600 1.00 13.61
ATOM 3044 CB HIS A 401 0 11.105 44.884 29.843 1.00 13.27
ATOM 3045 CG HIS A 401 0 10.184 44.441 28.751 1.00 14.50
15 ATOM 3046 ND1 HIS A 401 0 10.201 44.973 27.479 1.00 14.96
ATOM 3047 CD2 HIS A 401 0 9.202 43.492 28.750 1.00 12.35
ATOM 3048 CE1 HIS A 401 0 9.263 44.387 26.725 1.00 12.61
ATOM 3049 NE2 HIS A 401 0 8.677 43.507 27.492 1.00 12.41
ATOM 3050 N GLY A 402 0 14.103 44.549 30.855 1.00 15.59
20 ATOM 3051 CA GLY A 402 0 15.152 45.209 31.598 1.00 15.18
ATOM 3052 C GLY A 402 0 16.009 44.351 32.510 1.00 15.96
ATOM 3053 O GLY A 402 0 16.927 44.898 33.170 1.00 16.30
ATOM 3054 N HIS A 403 0 15.618 43.147 32.893 1.00 12.96
ATOM 3055 CA HIS A 403 0 16.282 42.337 33.873 1.00 15.00
25 ATOM 3056 C HIS A 403 0 16.226 40.839 33.586 1.00 15.22
ATOM 3057 O HIS A 403 0 15.253 40.381 32.971 1.00 16.16
ATOM 3058 CB HIS A 403 0 15.525 42.478 35.227 1.00 14.13
ATOM 3059 CG HIS A 403 0 15.571 43.829 35.827 1.00 16.69
ATOM 3060 ND1 HIS A 403 0 16.604 44.253 36.649 1.00 16.13
30 ATOM 3061 CD2 HIS A 403 0 14.744 44.911 35.659 1.00 15.50
ATOM 3062 CE1 HIS A 403 0 16.425 45.520 37.002 1.00 15.02
ATOM 3063 NE2 HIS A 403 0 15.285 45.905 36.430 1.00 16.15
ATOM 3064 N ALA A 404 0 17.138 40.054 34.113 1.00 13.71
ATOM 3065 CA ALA A 404 0 17.039 38.607 34.158 1.00 12.60
35 ATOM 3066 C ALA A 404 0 16.771 38.370 35.649 1.00 12.31
ATOM 3067 O ALA A 404 0 17.156 39.291 36.373 1.00 13.94
ATOM 3068 CB ALA A 404 0 18.249 37.819 33.721 1.00 13.84
ATOM 3069 N PHE A 405 0 16.085 37.356 36.126 1.00 12.21

ATOM 3070 CA PHE A 405 O 15.813 37.235 37.559 1.00 11.64
ATOM 3071 C PHE A 405 O 16.177 35.821 38.008 1.00 12.55
ATOM 3072 O PHE A 405 O 16.196 34.883 37.201 1.00 12.23
ATOM 3073 CB PHE A 405 O 14.325 37.487 37.907 1.00 11.82
5 ATOM 3074 CG PHE A 405 O 13.382 36.893 36.879 1.00 11.75
ATOM 3075 CD1 PHE A 405 O 13.030 35.557 36.933 1.00 10.76
ATOM 3076 CD2 PHE A 405 O 12.917 37.663 35.824 1.00 11.55
ATOM 3077 CE1 PHE A 405 O 12.189 35.002 35.978 1.00 11.52
ATOM 3078 CE2 PHE A 405 O 12.087 37.112 34.862 1.00 13.32
10 ATOM 3079 CZ PHE A 405 O 11.692 35.767 34.946 1.00 11.45
ATOM 3080 N SER A 406 O 16.414 35.625 39.288 1.00 12.86
ATOM 3081 CA SER A 406 O 16.660 34.286 39.796 1.00 13.43
ATOM 3082 C SER A 406 O 15.276 33.712 40.130 1.00 13.49
ATOM 3083 O SER A 406 O 14.518 34.375 40.847 1.00 10.13
15 ATOM 3084 CB SER A 406 O 17.433 34.290 41.123 1.00 13.78
ATOM 3085 OG SER A 406 O 18.708 34.834 40.938 1.00 16.72
ATOM 3086 N VAL A 407 O 15.100 32.453 39.741 1.00 14.53
ATOM 3087 CA VAL A 407 O 13.853 31.777 40.093 1.00 13.90
ATOM 3088 C VAL A 407 O 14.160 30.943 41.325 1.00 14.53
20 ATOM 3089 O VAL A 407 O 14.513 29.753 41.262 1.00 14.62
ATOM 3090 CB VAL A 407 O 13.333 30.903 38.941 1.00 16.43
ATOM 3091 CG1 VAL A 407 O 11.969 30.317 39.341 1.00 16.69
ATOM 3092 CG2 VAL A 407 O 13.272 31.682 37.626 1.00 14.90
ATOM 3093 N VAL A 408 O 13.971 31.544 42.485 1.00 14.32
25 ATOM 3094 CA VAL A 408 O 14.173 30.947 43.780 1.00 15.47
ATOM 3095 C VAL A 408 O 13.115 29.870 44.049 1.00 16.51
ATOM 3096 O VAL A 408 O 13.387 28.927 44.812 1.00 17.39
ATOM 3097 CB VAL A 408 O 14.280 31.967 44.932 1.00 15.75
ATOM 3098 CG1 VAL A 408 O 15.345 33.015 44.600 1.00 14.81
30 ATOM 3099 CG2 VAL A 408 O 12.952 32.693 45.189 1.00 15.99
ATOM 3100 N ARG A 409 O 11.972 29.940 43.387 1.00 16.28
ATOM 3101 CA ARG A 409 O 10.960 28.900 43.570 1.00 17.67
ATOM 3102 C ARG A 409 O 10.217 28.757 42.236 1.00 17.09
ATOM 3103 O ARG A 409 O 9.585 29.698 41.763 1.00 15.25
35 ATOM 3104 CB ARG A 409 O 9.993 29.143 44.718 1.00 17.87
ATOM 3105 CG ARG A 409 O 8.796 28.188 44.663 1.00 21.12
ATOM 3106 CD ARG A 409 O 8.008 28.181 45.945 1.00 22.10
ATOM 3107 NE ARG A 409 O 6.801 27.370 45.955 1.00 24.80

ATOM 3108 CZ ARG A 409 O 5.918 27.361 46.961 1.00 25.93
ATOM 3109 NH1 ARG A 409 O 4.859 26.569 46.877 1.00 27.14
ATOM 3110 NH2 ARG A 409 O 6.068 28.117 48.046 1.00 25.44
ATOM 3111 N SER A 410 O 10.366 27.576 41.668 1.00 16.33
5 ATOM 3112 CA SER A 410 O 9.802 27.245 40.373 1.00 18.33
ATOM 3113 C SER A 410 O 8.406 26.612 40.492 1.00 18.60
ATOM 3114 O SER A 410 O 7.941 26.223 41.566 1.00 16.94
ATOM 3115 CB SER A 410 O 10.724 26.199 39.705 1.00 19.51
ATOM 3116 OG SER A 410 O 11.718 26.865 38.933 1.00 20.28
10 ATOM 3117 N ALA A 411 O 7.754 26.551 39.343 1.00 18.19
ATOM 3118 CA ALA A 411 O 6.458 25.899 39.231 1.00 19.76
ATOM 3119 C ALA A 411 O 6.667 24.406 39.474 1.00 22.62
ATOM 3120 O ALA A 411 O 7.636 23.759 39.067 1.00 20.97
ATOM 3121 CB ALA A 411 O 5.873 26.075 37.841 1.00 17.13
15 ATOM 3122 N GLY A 412 O 5.710 23.856 40.229 1.00 26.30
ATOM 3123 CA GLY A 412 O 5.714 22.442 40.558 1.00 27.05
ATOM 3124 C GLY A 412 O 6.692 22.150 41.677 1.00 29.22
ATOM 3125 O GLY A 412 O 6.917 20.959 41.944 1.00 32.10
ATOM 3126 N SER A 413 O 7.293 23.139 42.322 1.00 28.66
20 ATOM 3127 CA SER A 413 O 8.223 22.871 43.400 1.00 28.58
ATOM 3128 C SER A 413 O 7.757 23.600 44.642 1.00 29.64
ATOM 3129 O SER A 413 O 7.279 24.735 44.524 1.00 30.66
ATOM 3130 CB SER A 413 O 9.610 23.407 43.015 1.00 30.12
ATOM 3131 OG SER A 413 O 10.484 23.233 44.127 1.00 31.74
25 ATOM 3132 N SER A 414 O 7.902 23.031 45.819 1.00 29.19
ATOM 3133 CA SER A 414 O 7.523 23.753 47.033 1.00 30.71
ATOM 3134 C SER A 414 O 8.762 24.124 47.834 1.00 30.51
ATOM 3135 O SER A 414 O 8.746 24.453 49.017 1.00 31.90
ATOM 3136 CB SER A 414 O 6.612 22.832 47.853 1.00 31.10
30 ATOM 3137 OG SER A 414 O 7.438 21.764 48.299 1.00 34.24
ATOM 3138 N THR A 415 O 9.919 24.063 47.194 1.00 30.60
ATOM 3139 CA THR A 415 O 11.194 24.336 47.860 1.00 30.60
ATOM 3140 C THR A 415 O 11.819 25.614 47.291 1.00 27.71
ATOM 3141 O THR A 415 O 11.582 25.998 46.137 1.00 27.49
35 ATOM 3142 CB THR A 415 O 12.089 23.095 47.747 1.00 32.16
ATOM 3143 OG1 THR A 415 O 13.411 23.441 47.285 1.00 35.60
ATOM 3144 CG2 THR A 415 O 11.599 22.103 46.710 1.00 34.11
ATOM 3145 N TYR A 416 O 12.662 26.268 48.053 1.00 24.34

ATOM 3146 CA TYR A 416 O 13.288 27.513 47.621 1.00 25.69
ATOM 3147 C TYR A 416 O 14.782 27.297 47.392 1.00 24.69
ATOM 3148 O TYR A 416 O 15.364 26.603 48.211 1.00 25.96
ATOM 3149 CB TYR A 416 O 13.129 28.633 48.659 1.00 23.79
5 ATOM 3150 CG TYR A 416 O 11.690 29.091 48.794 1.00 24.53
ATOM 3151 CD1 TYR A 416 O 10.789 28.387 49.596 1.00 24.14
ATOM 3152 CD2 TYR A 416 O 11.230 30.219 48.131 1.00 23.99
ATOM 3153 CE1 TYR A 416 O 9.474 28.799 49.713 1.00 23.70
ATOM 3154 CE2 TYR A 416 O 9.922 30.641 48.248 1.00 23.96
10 ATOM 3155 CZ TYR A 416 O 9.050 29.929 49.054 1.00 23.73
ATOM 3156 OH TYR A 416 O 7.744 30.337 49.152 1.00 23.53
ATOM 3157 N ASN A 417 O 15.360 27.867 46.353 1.00 22.34
ATOM 3158 CA ASN A 417 O 16.810 27.702 46.223 1.00 20.83
ATOM 3159 C ASN A 417 O 17.425 29.089 46.092 1.00 20.43
15 ATOM 3160 O ASN A 417 O 17.247 29.761 45.082 1.00 20.00
ATOM 3161 CB ASN A 417 O 17.179 26.763 45.086 1.00 19.72
ATOM 3162 CG ASN A 417 O 18.660 26.716 44.758 1.00 19.50
ATOM 3163 OD1 ASN A 417 O 19.485 27.313 45.465 1.00 20.18
ATOM 3164 ND2 ASN A 417 O 18.981 26.043 43.660 1.00 17.21
20 ATOM 3165 N PHE A 418 O 18.153 29.508 47.119 1.00 20.79
ATOM 3166 CA PHE A 418 O 18.831 30.797 47.049 1.00 20.77
ATOM 3167 C PHE A 418 O 20.314 30.613 46.725 1.00 20.47
ATOM 3168 O PHE A 418 O 20.973 31.618 46.517 1.00 19.47
ATOM 3169 CB PHE A 418 O 18.764 31.542 48.384 1.00 20.52
25 ATOM 3170 CG PHE A 418 O 17.332 31.821 48.753 1.00 22.19
ATOM 3171 CD1 PHE A 418 O 16.644 30.947 49.578 1.00 21.36
ATOM 3172 CD2 PHE A 418 O 16.697 32.951 48.244 1.00 21.95
ATOM 3173 CE1 PHE A 418 O 15.320 31.208 49.919 1.00 21.64
ATOM 3174 CE2 PHE A 418 O 15.386 33.198 48.599 1.00 22.81
30 ATOM 3175 CZ PHE A 418 O 14.694 32.325 49.419 1.00 22.57
ATOM 3176 N VAL A 419 O 20.816 29.380 46.732 1.00 19.72
ATOM 3177 CA VAL A 419 O 22.272 29.235 46.564 1.00 19.96
ATOM 3178 C VAL A 419 O 22.682 29.261 45.114 1.00 20.65
ATOM 3179 O VAL A 419 O 23.634 29.875 44.671 1.00 21.02
35 ATOM 3180 CB VAL A 419 O 22.708 27.888 47.200 1.00 21.81
ATOM 3181 CG1 VAL A 419 O 23.954 27.291 46.588 1.00 21.97
ATOM 3182 CG2 VAL A 419 O 22.885 28.098 48.713 1.00 21.55
ATOM 3183 N ASN A 420 O 21.867 28.585 44.327 1.00 19.77

ATOM 3184 CA ASN A 420 0 22.076 28.232 42.967 1.00 21.81
ATOM 3185 C ASN A 420 0 21.028 28.263 41.891 1.00 20.21
ATOM 3186 O ASN A 420 0 21.046 27.407 41.004 1.00 20.13
ATOM 3187 CB ASN A 420 0 22.166 26.587 43.207 1.00 21.91
5 ATOM 3188 CG ASN A 420 0 23.441 26.231 42.529 1.00 24.12
ATOM 3189 OD1 ASN A 420 0 23.933 25.113 42.403 1.00 26.75
ATOM 3190 ND2 ASN A 420 0 24.051 27.318 42.027 1.00 25.42
ATOM 3191 N PRO A 421 0 19.987 29.034 42.038 1.00 20.27
ATOM 3192 CA PRO A 421 0 18.808 28.951 41.183 1.00 17.57
10 ATOM 3193 C PRO A 421 0 19.100 29.369 39.778 1.00 15.76
ATOM 3194 O PRO A 421 0 19.907 30.281 39.586 1.00 15.13
ATOM 3195 CB PRO A 421 0 17.769 29.850 41.894 1.00 19.52
ATOM 3196 CG PRO A 421 0 18.674 30.863 42.589 1.00 19.88
ATOM 3197 CD PRO A 421 0 19.847 30.057 43.095 1.00 20.45
15 ATOM 3198 N VAL A 422 0 18.385 28.803 38.820 1.00 15.28
ATOM 3199 CA VAL A 422 0 18.502 29.239 37.420 1.00 13.48
ATOM 3200 C VAL A 422 0 18.157 30.721 37.397 1.00 14.53
ATOM 3201 O VAL A 422 0 17.340 31.208 38.183 1.00 14.44
ATOM 3202 CB VAL A 422 0 17.498 28.435 36.585 1.00 15.23
20 ATOM 3203 CG1 VAL A 422 0 16.032 28.747 36.937 1.00 13.85
ATOM 3204 CG2 VAL A 422 0 17.681 28.514 35.089 1.00 13.26
ATOM 3205 N LYS A 423 0 18.691 31.447 36.451 1.00 15.35
ATOM 3206 CA LYS A 423 0 18.366 32.831 36.189 1.00 17.23
ATOM 3207 C LYS A 423 0 17.759 32.891 34.784 1.00 16.55
25 ATOM 3208 O LYS A 423 0 18.284 32.189 33.909 1.00 16.92
ATOM 3209 CB LYS A 423 0 19.627 33.681 36.174 1.00 19.33
ATOM 3210 CG LYS A 423 0 20.118 33.985 37.565 1.00 24.09
ATOM 3211 CD LYS A 423 0 21.065 35.206 37.466 1.00 27.32
ATOM 3212 CE LYS A 423 0 22.470 34.596 37.263 1.00 28.78
30 ATOM 3213 NZ LYS A 423 0 23.128 34.482 38.595 1.00 29.50
ATOM 3214 N ARG A 424 0 16.630 33.570 34.617 1.00 15.85
ATOM 3215 CA ARG A 424 0 16.016 33.592 33.294 1.00 16.20
ATOM 3216 C ARG A 424 0 15.235 34.890 33.105 1.00 14.86
ATOM 3217 O ARG A 424 0 15.354 35.771 33.959 1.00 14.64
35 ATOM 3218 CB ARG A 424 0 15.158 32.367 32.994 1.00 16.11
ATOM 3219 CG ARG A 424 0 14.036 31.864 33.849 1.00 14.06
ATOM 3220 CD ARG A 424 0 13.447 30.506 33.427 1.00 11.65
ATOM 3221 NE ARG A 424 0 13.422 30.395 31.961 1.00 9.03

ATOM 3222 CZ ARG A 424 0 13.312 29.234 31.319 1.00 10.63
ATOM 3223 NH1 ARG A 424 0 13.185 28.133 32.082 1.00 11.02
ATOM 3224 NH2 ARG A 424 0 13.403 29.213 29.988 1.00 8.52
ATOM 3225 N ASP A 425 0 14.519 34.975 31.995 1.00 13.83
5 ATOM 3226 CA ASP A 425 0 13.751 36.209 31.752 1.00 15.00
ATOM 3227 C ASP A 425 0 12.298 35.929 31.359 1.00 15.65
ATOM 3228 O ASP A 425 0 11.474 36.850 31.271 1.00 15.11
ATOM 3229 CB ASP A 425 0 14.499 37.130 30.797 1.00 12.96
ATOM 3230 CG ASP A 425 0 14.609 36.652 29.371 1.00 14.32
10 ATOM 3231 OD1 ASP A 425 0 13.697 35.957 28.818 1.00 13.30
ATOM 3232 OD2 ASP A 425 0 15.632 37.003 28.729 1.00 13.76
ATOM 3233 N VAL A 426 0 11.883 34.675 31.206 1.00 15.21
ATOM 3234 CA VAL A 426 0 10.530 34.229 30.984 1.00 13.92
ATOM 3235 C VAL A 426 0 10.247 33.000 31.865 1.00 13.98
15 ATOM 3236 O VAL A 426 0 10.891 31.965 31.696 1.00 15.56
ATOM 3237 CB VAL A 426 0 10.128 33.807 29.567 1.00 12.49
ATOM 3238 CG1 VAL A 426 0 8.629 33.473 29.531 1.00 13.99
ATOM 3239 CG2 VAL A 426 0 10.390 34.874 28.536 1.00 12.37
ATOM 3240 N VAL A 427 0 9.274 33.090 32.766 1.00 12.82
20 ATOM 3241 CA VAL A 427 0 8.979 31.969 33.639 1.00 12.27
ATOM 3242 C VAL A 427 0 7.495 31.589 33.651 1.00 14.14
ATOM 3243 O VAL A 427 0 6.594 32.426 33.682 1.00 14.10
ATOM 3244 CB VAL A 427 0 9.458 32.315 35.056 1.00 11.46
ATOM 3245 CG1 VAL A 427 0 8.732 33.549 35.594 1.00 9.39
25 ATOM 3246 CG2 VAL A 427 0 9.353 31.116 35.982 1.00 10.53
ATOM 3247 N SER A 428 0 7.229 30.282 33.622 1.00 13.74
ATOM 3248 CA SER A 428 0 5.889 29.766 33.721 1.00 15.16
ATOM 3249 C SER A 428 0 5.445 29.878 35.171 1.00 15.48
ATOM 3250 O SER A 428 0 6.186 29.505 36.087 1.00 15.38
30 ATOM 3251 CB SER A 428 0 5.776 28.323 33.206 1.00 16.37
ATOM 3252 OG SER A 428 0 4.464 27.821 33.484 1.00 17.00
ATOM 3253 N LEU A 429 0 4.246 30.376 35.399 1.00 15.74
ATOM 3254 CA LEU A 429 0 3.686 30.489 36.744 1.00 15.73
ATOM 3255 C LEU A 429 0 3.035 29.184 37.198 1.00 16.41
35 ATOM 3256 O LEU A 429 0 2.741 29.041 38.390 1.00 15.74
ATOM 3257 CB LEU A 429 0 2.669 31.627 36.886 1.00 14.99
ATOM 3258 CG LEU A 429 0 3.155 33.027 36.540 1.00 16.60
ATOM 3259 CD1 LEU A 429 0 2.043 34.042 36.862 1.00 17.78

ATOM 3260 CD2 LEU A 429 O 4.438 33.386 37.281 1.00 16.26
ATOM 3261 N GLY A 430 O 2.913 28.218 36.295 1.00 17.70
ATOM 3262 CA GLY A 430 O 2.419 26.904 36.701 1.00 19.84
ATOM 3263 C GLY A 430 O 0.894 26.836 36.778 1.00 20.72
5 ATOM 3264 O GLY A 430 O 0.178 27.498 36.029 1.00 20.89
ATOM 3265 N VAL A 431 O 0.428 26.056 37.729 1.00 22.04
ATOM 3266 CA VAL A 431 O -0.956 25.713 37.966 1.00 22.61
ATOM 3267 C VAL A 431 O -1.337 26.028 39.409 1.00 23.06
ATOM 3268 O VAL A 431 O -0.476 26.392 40.218 1.00 22.42
10 ATOM 3269 CB VAL A 431 O -1.245 24.193 37.768 1.00 23.03
ATOM 3270 CG1 VAL A 431 O -0.795 23.672 36.416 1.00 22.74
ATOM 3271 CG2 VAL A 431 O -0.574 23.315 38.820 1.00 22.77
ATOM 3272 N THR A 432 O -2.615 25.835 39.704 1.00 23.88
ATOM 3273 CA THR A 432 O -3.168 26.067 41.041 1.00 24.18
15 ATOM 3274 C THR A 432 O -2.324 25.401 42.092 1.00 23.94
ATOM 3275 O THR A 432 O -1.915 24.249 41.909 1.00 24.69
ATOM 3276 CB THR A 432 O -4.625 25.565 41.069 1.00 25.75
ATOM 3277 OG1 THR A 432 O -5.336 26.344 40.087 1.00 25.87
ATOM 3278 CG2 THR A 432 O -5.319 25.800 42.398 1.00 26.65
20 ATOM 3279 N GLY A 433 O -1.924 26.136 43.124 1.00 24.45
ATOM 3280 CA GLY A 433 O -1.035 25.589 44.159 1.00 22.27
ATOM 3281 C GLY A 433 O 0.394 26.120 43.983 1.00 23.26
ATOM 3282 O GLY A 433 O 1.103 26.212 45.000 1.00 23.30
ATOM 3283 N ASP A 434 O 0.833 26.481 42.776 1.00 21.12
25 ATOM 3284 CA ASP A 434 O 2.192 26.986 42.586 1.00 20.62
ATOM 3285 C ASP A 434 O 2.360 28.408 43.126 1.00 22.36
ATOM 3286 O ASP A 434 O 1.425 29.225 43.076 1.00 21.24
ATOM 3287 CB ASP A 434 O 2.548 27.024 41.087 1.00 18.78
ATOM 3288 CG ASP A 434 O 2.827 25.616 40.597 1.00 19.71
30 ATOM 3289 OD1 ASP A 434 O 3.304 24.828 41.409 1.00 20.43
ATOM 3290 OD2 ASP A 434 O 2.596 25.242 39.432 1.00 21.58
ATOM 3291 N GLU A 435 O 3.585 28.721 43.562 1.00 22.08
ATOM 3292 CA GLU A 435 O 3.853 30.077 44.068 1.00 23.24
ATOM 3293 C GLU A 435 O 5.244 30.512 43.612 1.00 20.24
35 ATOM 3294 O GLU A 435 O 6.201 30.611 44.372 1.00 19.50
ATOM 3295 CB GLU A 435 O 3.659 30.068 45.572 1.00 25.56
ATOM 3296 CG GLU A 435 O 3.739 31.409 46.258 1.00 30.52
ATOM 3297 CD GLU A 435 O 3.107 31.350 47.657 1.00 35.00

ATOM 3298 OE1 GLU A 435 O 2.093 30.603 47.760 1.00 35.71
ATOM 3299 OE2 GLU A 435 O 3.658 32.020 48.579 1.00 35.91
ATOM 3300 N VAL A 436 O 5.344 30.690 42.297 1.00 17.80
ATOM 3301 CA VAL A 436 O 6.564 31.083 41.640 1.00 15.30
5 ATOM 3302 C VAL A 436 O 7.049 32.416 42.221 1.00 17.15
ATOM 3303 O VAL A 436 O 6.326 33.402 42.275 1.00 17.48
ATOM 3304 CB VAL A 436 O 6.360 31.219 40.129 1.00 14.63
ATOM 3305 CG1 VAL A 436 O 7.463 32.009 39.454 1.00 10.79
ATOM 3306 CG2 VAL A 436 O 6.238 29.806 39.536 1.00 14.13
10 ATOM 3307 N THR A 437 O 8.290 32.391 42.691 1.00 16.51
ATOM 3308 CA THR A 437 O 8.940 33.505 43.364 1.00 16.19
ATOM 3309 C THR A 437 O 10.254 33.817 42.668 1.00 15.24
ATOM 3310 O THR A 437 O 11.100 32.940 42.419 1.00 15.47
ATOM 3311 CB THR A 437 O 9.190 33.067 44.827 1.00 14.95
15 ATOM 3312 OG1 THR A 437 O 7.969 32.499 45.308 1.00 13.50
ATOM 3313 CG2 THR A 437 O 9.599 34.232 45.697 1.00 13.41
ATOM 3314 N ILE A 438 O 10.413 35.059 42.251 1.00 13.38
ATOM 3315 CA ILE A 438 O 11.597 35.471 41.510 1.00 15.78
ATOM 3316 C ILE A 438 O 12.292 36.590 42.264 1.00 15.86
20 ATOM 3317 O ILE A 438 O 11.617 37.270 43.048 1.00 17.32
ATOM 3318 CB ILE A 438 O 11.249 35.848 40.053 1.00 15.40
ATOM 3319 CG1 ILE A 438 O 10.340 37.055 39.985 1.00 15.85
ATOM 3320 CG2 ILE A 438 O 10.602 34.653 39.346 1.00 17.11
ATOM 3321 CD1 ILE A 438 O 9.971 37.607 38.632 1.00 17.49
25 ATOM 3322 N ARG A 439 O 13.599 36.789 42.055 1.00 16.02
ATOM 3323 CA ARG A 439 O 14.315 37.896 42.671 1.00 13.90
ATOM 3324 C ARG A 439 O 15.181 38.645 41.676 1.00 13.52
ATOM 3325 O ARG A 439 O 15.748 38.056 40.762 1.00 14.74
ATOM 3326 CB ARG A 439 O 15.193 37.501 43.850 1.00 15.15
30 ATOM 3327 CG ARG A 439 O 14.457 37.235 45.147 1.00 14.83
ATOM 3328 CD ARG A 439 O 15.367 37.337 46.355 1.00 14.08
ATOM 3329 NE ARG A 439 O 14.613 37.000 47.566 1.00 17.06
ATOM 3330 CZ ARG A 439 O 15.192 36.922 48.767 1.00 18.01
ATOM 3331 NH1 ARG A 439 O 16.487 37.176 48.908 1.00 17.76
35 ATOM 3332 NH2 ARG A 439 O 14.459 36.604 49.818 1.00 18.55
ATOM 3333 N PHE A 440 O 15.314 39.957 41.853 1.00 14.44
ATOM 3334 CA PHE A 440 O 16.204 40.737 40.993 1.00 15.97
ATOM 3335 C PHE A 440 O 16.645 41.986 41.761 1.00 15.86

ATOM 3336 O PHE A 440 0 16.113 42.313 42.801 1.00 15.79
ATOM 3337 CB PHE A 440 0 15.638 41.081 39.620 1.00 15.17
ATOM 3338 CG PHE A 440 0 14.416 41.948 39.647 1.00 16.95
ATOM 3339 CD1 PHE A 440 0 14.525 43.333 39.528 1.00 17.23
5 ATOM 3340 CD2 PHE A 440 0 13.158 41.377 39.798 1.00 16.35
ATOM 3341 CE1 PHE A 440 0 13.397 44.152 39.566 1.00 17.07
ATOM 3342 CE2 PHE A 440 0 12.026 42.180 39.841 1.00 17.12
ATOM 3343 CZ PHE A 440 0 12.144 43.575 39.719 1.00 18.30
ATOM 3344 N VAL A 441 0 17.676 42.648 41.268 1.00 16.10
10 ATOM 3345 CA VAL A 441 0 18.172 43.874 41.879 1.00 16.29
ATOM 3346 C VAL A 441 0 17.776 45.035 40.972 1.00 14.00
ATOM 3347 O VAL A 441 0 17.866 44.924 39.736 1.00 12.72
ATOM 3348 CB VAL A 441 0 19.675 43.769 42.144 1.00 18.13
ATOM 3349 CG1 VAL A 441 0 20.195 45.040 42.794 1.00 18.53
15 ATOM 3350 CG2 VAL A 441 0 19.969 42.583 43.065 1.00 18.55
ATOM 3351 N THR A 442 0 17.328 46.125 41.579 1.00 11.73
ATOM 3352 CA THR A 442 0 16.905 47.291 40.800 1.00 13.02
ATOM 3353 C THR A 442 0 18.055 48.208 40.432 1.00 14.83
ATOM 3354 O THR A 442 0 18.218 49.323 40.947 1.00 15.17
20 ATOM 3355 CB THR A 442 0 15.840 48.127 41.558 1.00 14.62
ATOM 3356 OG1 THR A 442 0 16.314 48.463 42.864 1.00 14.34
ATOM 3357 CG2 THR A 442 0 14.552 47.299 41.727 1.00 13.82
ATOM 3358 N ASP A 443 0 18.818 47.764 39.437 1.00 15.48
ATOM 3359 CA ASP A 443 0 20.004 48.449 38.964 1.00 16.57
25 ATOM 3360 C ASP A 443 0 19.807 49.010 37.569 1.00 15.38
ATOM 3361 O ASP A 443 0 20.788 49.208 36.858 1.00 15.57
ATOM 3362 CB ASP A 443 0 21.133 47.391 38.962 1.00 19.75
ATOM 3363 CG ASP A 443 0 20.877 46.264 37.990 1.00 22.78
ATOM 3364 OD1 ASP A 443 0 21.711 45.353 37.789 1.00 25.70
30 ATOM 3365 OD2 ASP A 443 0 19.836 46.161 37.313 1.00 23.88
ATOM 3366 N ASN A 444 0 18.593 49.278 37.144 1.00 13.71
ATOM 3367 CA ASN A 444 0 18.388 49.721 35.752 1.00 15.87
ATOM 3368 C ASN A 444 0 17.245 50.728 35.702 1.00 17.00
ATOM 3369 O ASN A 444 0 16.052 50.419 35.614 1.00 16.83
35 ATOM 3370 CB ASN A 444 0 18.198 48.453 34.930 1.00 15.78
ATOM 3371 CG ASN A 444 0 18.225 48.675 33.442 1.00 18.49
ATOM 3372 OD1 ASN A 444 0 18.505 49.809 33.047 1.00 19.42
ATOM 3373 ND2 ASN A 444 0 17.925 47.689 32.588 1.00 15.91

ATOM 3374 N PRO A 445 0 17.598 52.003 35.890 1.00 17.59
ATOM 3375 CA PRO A 445 0 16.683 53.137 35.938 1.00 16.56
ATOM 3376 C PRO A 445 0 15.788 53.217 34.721 1.00 16.99
ATOM 3377 O PRO A 445 0 16.293 53.246 33.594 1.00 17.02
5 ATOM 3378 CB PRO A 445 0 17.552 54.418 35.951 1.00 18.28
ATOM 3379 CG PRO A 445 0 18.870 53.871 36.474 1.00 18.09
ATOM 3380 CD PRO A 445 0 19.002 52.409 36.084 1.00 16.05
ATOM 3381 N GLY A 446 0 14.462 53.194 34.918 1.00 17.16
ATOM 3382 CA GLY A 446 0 13.560 53.281 33.743 1.00 15.84
10 ATOM 3383 C GLY A 446 0 12.297 52.453 33.984 1.00 14.24
ATOM 3384 O GLY A 446 0 12.192 51.797 35.005 1.00 12.22
ATOM 3385 N PRO A 447 0 11.285 52.697 33.181 1.00 15.53
ATOM 3386 CA PRO A 447 0 9.999 52.048 33.195 1.00 15.24
ATOM 3387 C PRO A 447 0 10.101 50.737 32.401 1.00 13.82
15 ATOM 3388 O PRO A 447 0 10.514 50.733 31.240 1.00 13.85
ATOM 3389 CB PRO A 447 0 9.013 52.976 32.473 1.00 16.21
ATOM 3390 CG PRO A 447 0 9.933 53.729 31.554 1.00 16.19
ATOM 3391 CD PRO A 447 0 11.347 53.707 32.096 1.00 17.15
ATOM 3392 N TRP A 448 0 9.787 49.623 33.021 1.00 11.83
20 ATOM 3393 CA TRP A 448 0 9.898 48.317 32.371 1.00 14.30
ATOM 3394 C TRP A 448 0 8.610 47.493 32.427 1.00 13.12
ATOM 3395 O TRP A 448 0 8.013 47.355 33.502 1.00 11.63
ATOM 3396 CB TRP A 448 0 10.985 47.483 33.095 1.00 13.17
ATOM 3397 CG TRP A 448 0 12.321 48.160 33.124 1.00 14.54
25 ATOM 3398 CD1 TRP A 448 0 12.897 48.728 34.239 1.00 14.19
ATOM 3399 CD2 TRP A 448 0 13.211 48.382 32.029 1.00 14.38
ATOM 3400 NE1 TRP A 448 0 14.083 49.290 33.873 1.00 15.02
ATOM 3401 CE2 TRP A 448 0 14.308 49.095 32.527 1.00 14.41
ATOM 3402 CE3 TRP A 448 0 13.193 48.053 30.672 1.00 15.39
30 ATOM 3403 CZ2 TRP A 448 0 15.388 49.467 31.729 1.00 14.57
ATOM 3404 CZ3 TRP A 448 0 14.250 48.446 29.867 1.00 14.92
ATOM 3405 CH2 TRP A 448 0 15.355 49.135 30.399 1.00 14.93
ATOM 3406 N PHE A 449 0 8.231 46.884 31.315 1.00 14.03
ATOM 3407 CA PHE A 449 0 7.023 46.039 31.297 1.00 13.60
35 ATOM 3408 C PHE A 449 0 7.231 44.712 32.016 1.00 15.32
ATOM 3409 O PHE A 449 0 8.312 44.093 31.993 1.00 13.66
ATOM 3410 CB PHE A 449 0 6.627 45.773 29.845 1.00 16.19
ATOM 3411 CG PHE A 449 0 5.221 46.033 29.380 1.00 18.26

	ATOM	3412	CD1	PHE	A 449	0	4.165	46.288	30.226	1.00	17.95
	ATOM	3413	CD2	PHE	A 449	0	4.962	46.027	28.011	1.00	20.73
	ATOM	3414	CE1	PHE	A 449	0	2.899	46.565	29.745	1.00	18.55
	ATOM	3415	CE2	PHE	A 449	0	3.701	46.293	27.503	1.00	20.13
5	ATOM	3416	CZ	PHE	A 449	0	2.664	46.543	28.387	1.00	18.59
	ATOM	3417	N	PHE	A 450	0	6.195	44.245	32.715	1.00	12.79
	ATOM	3418	CA	PHE	A 450	0	6.119	42.963	33.359	1.00	14.38
	ATOM	3419	C	PHE	A 450	0	4.775	42.323	32.952	1.00	15.45
	ATOM	3420	O	PHE	A 450	0	3.743	42.812	33.423	1.00	15.30
10	ATOM	3421	CB	PHE	A 450	0	6.186	43.041	34.879	1.00	15.06
	ATOM	3422	CG	PHE	A 450	0	6.210	41.693	35.555	1.00	15.95
	ATOM	3423	CD1	PHE	A 450	0	7.157	40.734	35.204	1.00	16.36
	ATOM	3424	CD2	PHE	A 450	0	5.325	41.398	36.570	1.00	15.45
	ATOM	3425	CE1	PHE	A 450	0	7.222	39.518	35.855	1.00	13.87
15	ATOM	3426	CE2	PHE	A 450	0	5.386	40.187	37.224	1.00	16.10
	ATOM	3427	CZ	PHE	A 450	0	6.317	39.236	36.854	1.00	15.90
	ATOM	3428	N	HIS	A 451	0	4.737	41.301	32.122	1.00	15.54
	ATOM	3429	CA	HIS	A 451	0	3.443	40.841	31.610	1.00	16.24
	ATOM	3430	C	HIS	A 451	0	3.461	39.426	31.073	1.00	16.95
20	ATOM	3431	O	HIS	A 451	0	4.526	38.860	30.812	1.00	17.42
	ATOM	3432	CB	HIS	A 451	0	2.996	41.743	30.435	1.00	14.01
	ATOM	3433	CG	HIS	A 451	0	3.921	41.696	29.281	1.00	16.98
	ATOM	3434	ND1	HIS	A 451	0	3.791	40.844	28.201	1.00	18.14
	ATOM	3435	CD2	HIS	A 451	0	5.058	42.435	29.046	1.00	17.88
25	ATOM	3436	CE1	HIS	A 451	0	4.759	41.060	27.337	1.00	17.83
	ATOM	3437	NE2	HIS	A 451	0	5.554	42.011	27.842	1.00	18.98
	ATOM	3438	N	CYS	A 452	0	2.261	38.863	30.951	1.00	16.78
	ATOM	3439	CA	CYS	A 452	0	2.167	37.537	30.388	1.00	16.34
	ATOM	3440	C	CYS	A 452	0	2.604	37.623	28.924	1.00	14.77
30	ATOM	3441	O	CYS	A 452	0	2.167	38.514	28.188	1.00	13.61
	ATOM	3442	CB	CYS	A 452	0	0.727	36.983	30.451	1.00	18.22
	ATOM	3443	SG	CYS	A 452	0	0.701	35.325	29.692	1.00	19.80
	ATOM	3444	N	HIS	A 453	0	3.388	36.640	28.474	1.00	13.29
	ATOM	3445	CA	HIS	A 453	0	3.867	36.716	27.100	1.00	13.19
35	ATOM	3446	C	HIS	A 453	0	2.983	35.987	26.099	1.00	13.47
	ATOM	3447	O	HIS	A 453	0	3.296	35.974	24.906	1.00	11.93
	ATOM	3448	CB	HIS	A 453	0	5.314	36.251	27.033	1.00	13.98
	ATOM	3449	CG	HIS	A 453	0	6.124	36.860	25.945	1.00	11.89

	ATOM	3450	ND1	HIS	A	453	0	5.835	36.763	24.612	1.00	10.68
	ATOM	3451	CD2	HIS	A	453	0	7.270	37.594	26.072	1.00	12.71
	ATOM	3452	CE1	HIS	A	453	0	6.776	37.418	23.923	1.00	12.37
	ATOM	3453	NE2	HIS	A	453	0	7.663	37.930	24.793	1.00	13.20
5	ATOM	3454	N	ILE	A	454	0	1.860	35.429	26.549	1.00	15.35
	ATOM	3455	CA	ILE	A	454	0	0.849	34.937	25.600	1.00	15.85
	ATOM	3456	C	ILE	A	454	0	0.214	36.238	25.089	1.00	18.65
	ATOM	3457	O	ILE	A	454	0	-0.452	36.997	25.824	1.00	17.92
	ATOM	3458	CB	ILE	A	454	0	-0.156	34.001	26.280	1.00	16.46
10	ATOM	3459	CG1	ILE	A	454	0	0.456	32.598	26.512	1.00	15.26
	ATOM	3460	CG2	ILE	A	454	0	-1.402	33.898	25.419	1.00	14.21
	ATOM	3461	CD1	ILE	A	454	0	-0.249	31.804	27.592	1.00	16.26
	ATOM	3462	N	GLU	A	455	0	0.448	36.607	23.832	1.00	21.02
	ATOM	3463	CA	GLU	A	455	0	-0.024	37.856	23.289	1.00	23.78
15	ATOM	3464	C	GLU	A	455	0	-1.526	38.042	23.422	1.00	24.40
	ATOM	3465	O	GLU	A	455	0	-1.953	39.161	23.700	1.00	24.30
	ATOM	3466	CB	GLU	A	455	0	0.399	38.090	21.830	1.00	27.20
	ATOM	3467	CG	GLU	A	455	0	0.602	39.599	21.595	1.00	33.86
	ATOM	3468	CD	GLU	A	455	0	1.783	40.205	22.309	1.00	37.49
20	ATOM	3469	OE1	GLU	A	455	0	2.311	39.657	23.320	1.00	41.51
	ATOM	3470	OE2	GLU	A	455	0	2.303	41.284	21.907	1.00	41.22
	ATOM	3471	N	PHE	A	456	0	-2.347	37.005	23.334	1.00	23.97
	ATOM	3472	CA	PHE	A	456	0	-3.775	37.163	23.516	1.00	24.68
	ATOM	3473	C	PHE	A	456	0	-4.084	37.533	24.959	1.00	25.11
25	ATOM	3474	O	PHE	A	456	0	-5.181	38.092	25.170	1.00	27.37
	ATOM	3475	CB	PHE	A	456	0	-4.552	35.919	23.023	1.00	24.76
	ATOM	3476	CG	PHE	A	456	0	-4.098	35.614	21.606	1.00	24.98
	ATOM	3477	CD1	PHE	A	456	0	-4.392	36.500	20.590	1.00	24.98
	ATOM	3478	CD2	PHE	A	456	0	-3.331	34.506	21.320	1.00	24.42
30	ATOM	3479	CE1	PHE	A	456	0	-3.988	36.292	19.291	1.00	25.44
	ATOM	3480	CE2	PHE	A	456	0	-2.913	34.293	20.015	1.00	26.40
	ATOM	3481	CZ	PHE	A	456	0	-3.226	35.171	18.997	1.00	25.10
	ATOM	3482	N	HIS	A	457	0	-3.205	37.294	25.922	1.00	22.35
	ATOM	3483	CA	HIS	A	457	0	-3.508	37.682	27.291	1.00	22.55
35	ATOM	3484	C	HIS	A	457	0	-3.053	39.121	27.561	1.00	23.81
	ATOM	3485	O	HIS	A	457	0	-3.756	39.832	28.262	1.00	21.33
	ATOM	3486	CB	HIS	A	457	0	-2.912	36.766	28.336	1.00	20.96
	ATOM	3487	CG	HIS	A	457	0	-3.345	35.346	28.201	1.00	22.51

ATOM 3488 ND1 HIS A 457 0 -2.745 34.329 28.905 1.00 21.40
ATOM 3489 CD2 HIS A 457 0 -4.291 34.771 27.404 1.00 22.50
ATOM 3490 CE1 HIS A 457 0 -3.320 33.184 28.575 1.00 22.51
ATOM 3491 NE2 HIS A 457 0 -4.237 33.428 27.666 1.00 23.19
5 ATOM 3492 N LEU A 458 0 -1.876 39.481 27.028 1.00 23.74
ATOM 3493 CA LEU A 458 0 -1.357 40.817 27.125 1.00 24.76
ATOM 3494 C LEU A 458 0 -2.411 41.828 26.616 1.00 26.52
ATOM 3495 O LEU A 458 0 -2.757 42.751 27.351 1.00 25.18
ATOM 3496 CB LEU A 458 0 -0.108 40.986 26.252 1.00 23.81
10 ATOM 3497 CG LEU A 458 0 0.898 42.062 26.624 1.00 24.09
ATOM 3498 CD1 LEU A 458 0 1.619 42.606 25.390 1.00 24.28
ATOM 3499 CD2 LEU A 458 0 0.351 43.195 27.462 1.00 23.72
ATOM 3500 N MET A 459 0 -2.896 41.611 25.388 1.00 28.19
ATOM 3501 CA MET A 459 0 -3.914 42.458 24.785 1.00 31.98
15 ATOM 3502 C MET A 459 0 -5.207 42.436 25.603 1.00 29.95
ATOM 3503 O MET A 459 0 -5.886 43.439 25.520 1.00 29.10
ATOM 3504 CB MET A 459 0 -4.148 42.226 23.284 1.00 35.99
ATOM 3505 CG MET A 459 0 -5.056 41.103 22.852 1.00 42.66
ATOM 3506 SD MET A 459 0 -5.296 40.817 21.069 1.00 49.28
20 ATOM 3507 CE MET A 459 0 -6.238 39.291 21.119 1.00 47.39
ATOM 3508 N ASN A 460 0 -5.523 41.486 26.464 1.00 29.07
ATOM 3509 CA ASN A 460 0 -6.706 41.539 27.296 1.00 29.41
ATOM 3510 C ASN A 460 0 -6.407 41.908 28.746 1.00 28.46
ATOM 3511 O ASN A 460 0 -7.183 41.577 29.645 1.00 26.89
25 ATOM 3512 CB ASN A 460 0 -7.537 40.253 27.210 1.00 31.34
ATOM 3513 CG ASN A 460 0 -8.325 40.243 25.900 1.00 33.82
ATOM 3514 OD1 ASN A 460 0 -7.909 39.609 24.926 1.00 34.29
ATOM 3515 ND2 ASN A 460 0 -9.437 40.971 25.861 1.00 34.55
ATOM 3516 N GLY A 461 0 -5.320 42.655 28.981 1.00 26.30
30 ATOM 3517 CA GLY A 461 0 -5.020 43.198 30.268 1.00 24.99
ATOM 3518 C GLY A 461 0 -4.043 42.601 31.235 1.00 24.75
ATOM 3519 O GLY A 461 0 -3.879 43.228 32.304 1.00 22.69
ATOM 3520 N LEU A 462 0 -3.375 41.478 30.914 1.00 22.85
ATOM 3521 CA LEU A 462 0 -2.478 40.872 31.913 1.00 22.10
35 ATOM 3522 C LEU A 462 0 -1.071 41.485 31.890 1.00 21.56
ATOM 3523 O LEU A 462 0 -0.116 40.876 31.415 1.00 20.28
ATOM 3524 CB LEU A 462 0 -2.477 39.376 31.669 1.00 20.03
ATOM 3525 CG LEU A 462 0 -2.010 38.393 32.720 1.00 20.40

	ATOM	3526	CD1	LEU	A 462	0	-2.603	38.608	34.093	1.00	20.35
	ATOM	3527	CD2	LEU	A 462	0	-2.385	36.983	32.229	1.00	21.01
	ATOM	3528	N	ALA	A 463	0	-0.908	42.695	32.408	1.00	20.00
	ATOM	3529	CA	ALA	A 463	0	0.350	43.432	32.381	1.00	20.74
5	ATOM	3530	C	ALA	A 463	0	0.398	44.511	33.481	1.00	21.85
	ATOM	3531	O	ALA	A 463	0	-0.667	44.965	33.934	1.00	22.85
	ATOM	3532	CB	ALA	A 463	0	0.559	44.179	31.060	1.00	15.13
	ATOM	3533	N	ILE	A 464	0	1.605	44.810	33.950	1.00	19.91
	ATOM	3534	CA	ILE	A 464	0	1.852	45.905	34.850	1.00	19.81
10	ATOM	3535	C	ILE	A 464	0	3.180	46.579	34.434	1.00	19.41
	ATOM	3536	O	ILE	A 464	0	3.938	46.003	33.660	1.00	18.24
	ATOM	3537	CB	ILE	A 464	0	1.910	45.678	36.347	1.00	19.13
	ATOM	3538	CG1	ILE	A 464	0	2.867	44.546	36.697	1.00	19.39
	ATOM	3539	CG2	ILE	A 464	0	0.520	45.455	36.924	1.00	18.48
15	ATOM	3540	CD1	ILE	A 464	0	3.205	44.549	38.179	1.00	21.00
	ATOM	3541	N	VAL	A 465	0	3.380	47.791	34.924	1.00	18.95
	ATOM	3542	CA	VAL	A 465	0	4.579	48.570	34.637	1.00	18.36
	ATOM	3543	C	VAL	A 465	0	5.327	48.928	35.931	1.00	18.07
	ATOM	3544	O	VAL	A 465	0	4.787	49.424	36.931	1.00	15.19
20	ATOM	3545	CB	VAL	A 465	0	4.329	49.913	33.918	1.00	19.73
	ATOM	3546	CG1	VAL	A 465	0	5.659	50.605	33.602	1.00	18.34
	ATOM	3547	CG2	VAL	A 465	0	3.522	49.766	32.629	1.00	18.74
	ATOM	3548	N	PHE	A 466	0	6.649	48.655	35.879	1.00	17.55
	ATOM	3549	CA	PHE	A 466	0	7.499	49.051	37.013	1.00	14.72
25	ATOM	3550	C	PHE	A 466	0	8.251	50.344	36.653	1.00	12.68
	ATOM	3551	O	PHE	A 466	0	9.007	50.420	35.679	1.00	12.23
	ATOM	3552	CB	PHE	A 466	0	8.484	47.978	37.381	1.00	15.19
	ATOM	3553	CG	PHE	A 466	0	7.962	46.770	38.080	1.00	15.90
	ATOM	3554	CD1	PHE	A 466	0	7.328	46.856	39.299	1.00	16.23
30	ATOM	3555	CD2	PHE	A 466	0	8.153	45.533	37.492	1.00	16.23
	ATOM	3556	CE1	PHE	A 466	0	6.861	45.720	39.936	1.00	15.97
	ATOM	3557	CE2	PHE	A 466	0	7.665	44.389	38.133	1.00	18.27
	ATOM	3558	CZ	PHE	A 466	0	7.018	44.480	39.352	1.00	16.74
	ATOM	3559	N	ALA	A 467	0	8.045	51.361	37.443	1.00	10.60
35	ATOM	3560	CA	ALA	A 467	0	8.788	52.648	37.194	1.00	12.27
	ATOM	3561	C	ALA	A 467	0	10.007	52.526	38.111	1.00	12.02
	ATOM	3562	O	ALA	A 467	0	9.905	52.728	39.325	1.00	12.43
	ATOM	3563	CB	ALA	A 467	0	7.845	53.790	37.501	1.00	10.50

ATOM 3564 N GLU A 468 0 11.126 51.989 37.625 1.00 12.62
ATOM 3565 CA GLU A 468 0 12.263 51.683 38.515 1.00 14.63
ATOM 3566 C GLU A 468 0 13.195 52.883 38.685 1.00 13.91
ATOM 3567 O GLU A 468 0 13.631 53.369 37.651 1.00 13.05
5 ATOM 3568 CB GLU A 468 0 13.049 50.546 37.843 1.00 14.51
ATOM 3569 CG GLU A 468 0 14.256 50.035 38.629 1.00 16.84
ATOM 3570 CD GLU A 468 0 14.805 48.779 37.975 1.00 17.96
ATOM 3571 OE1 GLU A 468 0 15.985 48.479 38.124 1.00 16.98
ATOM 3572 OE2 GLU A 468 0 14.086 48.043 37.260 1.00 18.42
10 ATOM 3573 N ASP A 469 0 13.546 53.286 39.886 1.00 15.17
ATOM 3574 CA ASP A 469 0 14.491 54.371 40.116 1.00 16.85
ATOM 3575 C ASP A 469 0 14.134 55.630 39.333 1.00 16.33
ATOM 3576 O ASP A 469 0 14.851 56.046 38.437 1.00 16.59
ATOM 3577 CB ASP A 469 0 15.899 53.920 39.748 1.00 19.86
15 ATOM 3578 CG ASP A 469 0 17.040 54.766 40.289 1.00 21.40
ATOM 3579 OD1 ASP A 469 0 16.811 55.793 40.943 1.00 22.21
ATOM 3580 OD2 ASP A 469 0 18.216 54.403 40.069 1.00 22.21
ATOM 3581 N MET A 470 0 13.007 56.246 39.635 1.00 16.12
ATOM 3582 CA MET A 470 0 12.522 57.373 38.853 1.00 18.77
20 ATOM 3583 C MET A 470 0 13.451 58.576 38.950 1.00 16.31
ATOM 3584 O MET A 470 0 13.591 59.208 37.925 1.00 13.55
ATOM 3585 CB MET A 470 0 11.116 57.847 39.302 1.00 20.06
ATOM 3586 CG MET A 470 0 10.041 56.941 38.684 1.00 23.99
ATOM 3587 SD MET A 470 0 8.375 57.337 39.283 1.00 26.08
25 ATOM 3588 CE MET A 470 0 8.030 58.581 38.020 1.00 24.40
ATOM 3589 N ALA A 471 0 14.046 58.793 40.117 1.00 14.69
ATOM 3590 CA ALA A 471 0 14.953 59.906 40.287 1.00 16.97
ATOM 3591 C ALA A 471 0 16.141 59.864 39.335 1.00 18.79
ATOM 3592 O ALA A 471 0 16.602 60.956 38.945 1.00 21.08
30 ATOM 3593 CB ALA A 471 0 15.471 59.927 41.728 1.00 17.62
ATOM 3594 N ASN A 472 0 16.623 58.695 38.912 1.00 17.28
ATOM 3595 CA ASN A 472 0 17.788 58.675 38.015 1.00 16.56
ATOM 3596 C ASN A 472 0 17.457 58.355 36.572 1.00 16.99
ATOM 3597 O ASN A 472 0 18.407 58.143 35.795 1.00 18.74
35 ATOM 3598 CB ASN A 472 0 18.811 57.645 38.548 1.00 14.60
ATOM 3599 CG ASN A 472 0 19.417 58.132 39.887 1.00 14.00
ATOM 3600 OD1 ASN A 472 0 18.895 57.830 40.967 1.00 12.71
ATOM 3601 ND2 ASN A 472 0 20.468 58.916 39.775 1.00 10.80

ATOM 3602 N THR A 473 O 16.174 58.284 36.239 1.00 14.26
ATOM 3603 CA THR A 473 O 15.789 57.885 34.882 1.00 15.82
ATOM 3604 C THR A 473 O 16.150 58.891 33.812 1.00 16.81
ATOM 3605 O THR A 473 O 16.599 58.455 32.746 1.00 15.89
5 ATOM 3606 CB THR A 473 O 14.267 57.576 34.826 1.00 16.10
ATOM 3607 OG1 THR A 473 O 14.001 56.416 35.609 1.00 15.41
ATOM 3608 CG2 THR A 473 O 13.750 57.337 33.427 1.00 15.24
ATOM 3609 N VAL A 474 O 16.000 60.195 34.081 1.00 18.57
ATOM 3610 CA VAL A 474 O 16.355 61.192 33.050 1.00 21.06
10 ATOM 3611 C VAL A 474 O 17.859 61.209 32.817 1.00 19.12
ATOM 3612 O VAL A 474 O 18.339 61.234 31.688 1.00 19.95
ATOM 3613 CB VAL A 474 O 15.860 62.616 33.424 1.00 22.91
ATOM 3614 CG1 VAL A 474 O 16.467 63.702 32.538 1.00 23.06
ATOM 3615 CG2 VAL A 474 O 14.346 62.721 33.334 1.00 23.04
15 ATOM 3616 N ASP A 475 O 18.647 61.175 33.886 1.00 19.20
ATOM 3617 CA ASP A 475 O 20.109 61.168 33.741 1.00 18.98
ATOM 3618 C ASP A 475 O 20.578 59.899 33.047 1.00 17.52
ATOM 3619 O ASP A 475 O 21.386 60.028 32.130 1.00 18.31
ATOM 3620 CB ASP A 475 O 20.780 61.273 35.119 1.00 20.27
20 ATOM 3621 CG ASP A 475 O 22.283 61.075 35.107 1.00 20.18
ATOM 3622 OD1 ASP A 475 O 22.950 61.889 34.431 1.00 21.73
ATOM 3623 OD2 ASP A 475 O 22.798 60.139 35.750 1.00 18.03
ATOM 3624 N ALA A 476 O 20.062 58.725 33.392 1.00 18.26
ATOM 3625 CA ALA A 476 O 20.539 57.486 32.793 1.00 18.93
25 ATOM 3626 C ALA A 476 O 20.165 57.269 31.343 1.00 20.62
ATOM 3627 O ALA A 476 O 20.845 56.502 30.661 1.00 22.64
ATOM 3628 CB ALA A 476 O 19.966 56.298 33.551 1.00 18.48
ATOM 3629 N ASN A 477 O 19.047 57.787 30.858 1.00 22.66
ATOM 3630 CA ASN A 477 O 18.605 57.512 29.491 1.00 25.22
30 ATOM 3631 C ASN A 477 O 18.578 58.782 28.683 1.00 28.55
ATOM 3632 O ASN A 477 O 17.969 59.755 29.143 1.00 30.20
ATOM 3633 CB ASN A 477 O 17.172 56.948 29.560 1.00 24.22
ATOM 3634 CG ASN A 477 O 17.114 55.666 30.380 1.00 23.73
ATOM 3635 OD1 ASN A 477 O 16.747 55.672 31.570 1.00 21.33
35 ATOM 3636 ND2 ASN A 477 O 17.512 54.575 29.736 1.00 20.87
ATOM 3637 N ASN A 478 O 19.208 58.878 27.514 1.00 31.69
ATOM 3638 CA ASN A 478 O 19.036 60.131 26.776 1.00 33.61
ATOM 3639 C ASN A 478 O 18.758 59.770 25.331 1.00 32.22

ATOM 3640 O ASN A 478 0 19.602 59.478 24.508 1.00 32.16
ATOM 3641 CB ASN A 478 0 20.086 61.194 27.017 1.00 38.57
ATOM 3642 CG ASN A 478 0 21.426 60.602 27.370 1.00 40.94
ATOM 3643 OD1 ASN A 478 0 21.928 59.903 26.484 1.00 44.60
5 ATOM 3644 ND2 ASN A 478 0 21.866 60.861 28.578 1.00 41.32
ATOM 3645 N PRO A 479 0 17.461 59.733 25.075 1.00 32.37
ATOM 3646 CA PRO A 479 0 16.890 59.381 23.790 1.00 31.84
ATOM 3647 C PRO A 479 0 17.268 60.448 22.776 1.00 32.35
ATOM 3648 O PRO A 479 0 17.422 61.609 23.136 1.00 32.66
10 ATOM 3649 CB PRO A 479 0 15.364 59.385 23.931 1.00 31.68
ATOM 3650 CG PRO A 479 0 15.126 59.724 25.373 1.00 31.69
ATOM 3651 CD PRO A 479 0 16.416 60.071 26.064 1.00 32.23
ATOM 3652 N PRO A 480 0 17.399 60.036 21.537 1.00 31.62
ATOM 3653 CA PRO A 480 0 17.670 60.939 20.422 1.00 30.72
15 ATOM 3654 C PRO A 480 0 16.452 61.827 20.225 1.00 30.37
ATOM 3655 O PRO A 480 0 15.362 61.525 20.733 1.00 29.47
ATOM 3656 CB PRO A 480 0 17.935 60.035 19.203 1.00 29.87
ATOM 3657 CG PRO A 480 0 17.111 58.811 19.590 1.00 30.44
ATOM 3658 CD PRO A 480 0 17.161 58.657 21.093 1.00 30.35
20 ATOM 3659 N VAL A 481 0 16.559 62.906 19.458 1.00 31.72
ATOM 3660 CA VAL A 481 0 15.398 63.788 19.268 1.00 30.68
ATOM 3661 C VAL A 481 0 14.335 63.090 18.446 1.00 29.51
ATOM 3662 O VAL A 481 0 13.134 63.284 18.648 1.00 27.97
ATOM 3663 CB VAL A 481 0 15.818 65.132 18.648 1.00 33.04
25 ATOM 3664 CG1 VAL A 481 0 16.126 65.010 17.161 1.00 31.91
ATOM 3665 CG2 VAL A 481 0 14.717 66.171 18.907 1.00 33.32
ATOM 3666 N GLU A 482 0 14.746 62.167 17.562 1.00 28.90
ATOM 3667 CA GLU A 482 0 13.755 61.402 16.803 1.00 29.62
ATOM 3668 C GLU A 482 0 12.839 60.565 17.691 1.00 28.33
30 ATOM 3669 O GLU A 482 0 11.704 60.287 17.280 1.00 28.36
ATOM 3670 CB GLU A 482 0 14.449 60.498 15.788 1.00 30.63
ATOM 3671 CG GLU A 482 0 15.143 61.256 14.666 1.00 32.78
ATOM 3672 CD GLU A 482 0 16.522 61.784 14.990 1.00 34.96
ATOM 3673 OE1 GLU A 482 0 17.021 61.746 16.141 1.00 34.62
35 ATOM 3674 OE2 GLU A 482 0 17.170 62.297 14.033 1.00 37.13
ATOM 3675 N TRP A 483 0 13.311 60.124 18.857 1.00 25.91
ATOM 3676 CA TRP A 483 0 12.496 59.280 19.711 1.00 25.49
ATOM 3677 C TRP A 483 0 11.224 60.011 20.125 1.00 26.47

	ATOM	3678	O	TRP A 483	0	10.155	59.405	20.116	1.00	26.95
	ATOM	3679	CB	TRP A 483	0	13.216	58.807	20.974	1.00	21.98
	ATOM	3680	CG	TRP A 483	0	12.376	58.144	22.013	1.00	21.49
	ATOM	3681	CD1	TRP A 483	0	11.960	56.827	22.003	1.00	20.81
5	ATOM	3682	CD2	TRP A 483	0	11.818	58.730	23.194	1.00	20.14
	ATOM	3683	NE1	TRP A 483	0	11.187	56.575	23.143	1.00	20.29
	ATOM	3684	CE2	TRP A 483	0	11.097	57.736	23.868	1.00	20.29
	ATOM	3685	CE3	TRP A 483	0	11.875	60.006	23.754	1.00	21.32
	ATOM	3686	CZ2	TRP A 483	0	10.422	57.973	25.062	1.00	20.89
10	ATOM	3687	CZ3	TRP A 483	0	11.217	60.248	24.946	1.00	20.78
	ATOM	3688	CH2	TRP A 483	0	10.495	59.227	25.596	1.00	21.44
	ATOM	3689	N	ALA A 484	0	11.342	61.261	20.560	1.00	28.59
	ATOM	3690	CA	ALA A 484	0	10.165	62.003	21.029	1.00	30.73
	ATOM	3691	C	ALA A 484	0	9.226	62.350	19.869	1.00	30.42
15	ATOM	3692	O	ALA A 484	0	8.024	62.337	20.071	1.00	31.34
	ATOM	3693	CB	ALA A 484	0	10.583	63.244	21.806	1.00	31.05
	ATOM	3694	N	GLN A 485	0	9.702	62.488	18.653	1.00	30.79
	ATOM	3695	CA	GLN A 485	0	8.927	62.742	17.466	1.00	33.16
	ATOM	3696	C	GLN A 485	0	8.026	61.608	17.017	1.00	32.81
20	ATOM	3697	O	GLN A 485	0	7.044	61.847	16.302	1.00	32.74
	ATOM	3698	CB	GLN A 485	0	9.859	63.113	16.290	1.00	34.56
	ATOM	3699	CG	GLN A 485	0	10.631	64.361	16.686	1.00	39.67
	ATOM	3700	CD	GLN A 485	0	11.559	64.919	15.640	1.00	42.86
	ATOM	3701	OE1	GLN A 485	0	11.528	66.145	15.434	1.00	45.48
25	ATOM	3702	NE2	GLN A 485	0	12.375	64.103	14.982	1.00	44.07
	ATOM	3703	N	LEU A 486	0	8.328	60.380	17.443	1.00	30.46
	ATOM	3704	CA	LEU A 486	0	7.500	59.231	17.095	1.00	27.76
	ATOM	3705	C	LEU A 486	0	6.051	59.510	17.509	1.00	28.23
	ATOM	3706	O	LEU A 486	0	5.100	59.331	16.752	1.00	26.71
30	ATOM	3707	CB	LEU A 486	0	8.043	58.034	17.838	1.00	25.03
	ATOM	3708	CG	LEU A 486	0	8.988	57.012	17.226	1.00	24.18
	ATOM	3709	CD1	LEU A 486	0	9.780	57.416	16.011	1.00	21.41
	ATOM	3710	CD2	LEU A 486	0	9.864	56.464	18.342	1.00	23.28
	ATOM	3711	N	CYS A 487	0	5.870	59.974	18.739	1.00	28.05
35	ATOM	3712	CA	CYS A 487	0	4.560	60.263	19.279	1.00	30.77
	ATOM	3713	C	CYS A 487	0	3.823	61.350	18.499	1.00	33.19
	ATOM	3714	O	CYS A 487	0	2.627	61.170	18.263	1.00	33.69
	ATOM	3715	CB	CYS A 487	0	4.643	60.637	20.752	1.00	27.94

	ATOM	3716	SG	CYS A 487	0	5.214	59.280	21.781	1.00	27.23
	ATOM	3717	N	GLU A 488	0	4.543	62.373	18.064	1.00	35.80
	ATOM	3718	CA	GLU A 488	0	3.871	63.458	17.334	1.00	39.12
	ATOM	3719	C	GLU A 488	0	3.384	62.928	15.995	1.00	37.78
5	ATOM	3720	O	GLU A 488	0	2.186	63.025	15.711	1.00	37.61
	ATOM	3721	CB	GLU A 488	0	4.737	64.697	17.257	1.00	42.04
	ATOM	3722	CG	GLU A 488	0	5.667	64.822	16.064	1.00	47.75
	ATOM	3723	CD	GLU A 488	0	5.634	66.239	15.500	1.00	51.36
	ATOM	3724	OE1	GLU A 488	0	5.501	66.422	14.266	1.00	52.66
10	ATOM	3725	OE2	GLU A 488	0	5.743	67.154	16.358	1.00	53.40
	ATOM	3726	N	ILE A 489	0	4.263	62.253	15.267	1.00	36.63
	ATOM	3727	CA	ILE A 489	0	3.906	61.647	14.004	1.00	36.74
	ATOM	3728	C	ILE A 489	0	2.754	60.662	14.113	1.00	36.98
	ATOM	3729	O	ILE A 489	0	1.847	60.664	13.276	1.00	38.60
15	ATOM	3730	CB	ILE A 489	0	5.089	60.903	13.361	1.00	36.57
	ATOM	3731	CG1	ILE A 489	0	6.267	61.853	13.148	1.00	36.46
	ATOM	3732	CG2	ILE A 489	0	4.651	60.305	12.030	1.00	36.90
	ATOM	3733	CD1	ILE A 489	0	7.535	61.194	12.654	1.00	35.62
	ATOM	3734	N	TYR A 490	0	2.758	59.808	15.105	1.00	36.22
20	ATOM	3735	CA	TYR A 490	0	1.771	58.765	15.298	1.00	35.95
	ATOM	3736	C	TYR A 490	0	0.413	59.314	15.692	1.00	37.83
	ATOM	3737	O	TYR A 490	0	-0.581	58.816	15.165	1.00	39.24
	ATOM	3738	CB	TYR A 490	0	2.206	57.817	16.409	1.00	32.47
	ATOM	3739	CG	TYR A 490	0	1.314	56.641	16.663	1.00	30.55
25	ATOM	3740	CD1	TYR A 490	0	1.176	55.623	15.726	1.00	29.96
	ATOM	3741	CD2	TYR A 490	0	0.610	56.536	17.849	1.00	29.79
	ATOM	3742	CE1	TYR A 490	0	0.378	54.528	15.975	1.00	29.51
	ATOM	3743	CE2	TYR A 490	0	-0.192	55.441	18.114	1.00	29.64
	ATOM	3744	CZ	TYR A 490	0	-0.288	54.445	17.171	1.00	29.51
30	ATOM	3745	OH	TYR A 490	0	-1.101	53.363	17.437	1.00	32.06
	ATOM	3746	N	ASP A 491	0	0.369	60.302	16.564	1.00	40.86
	ATOM	3747	CA	ASP A 491	0	-0.909	60.887	16.963	1.00	43.97
	ATOM	3748	C	ASP A 491	0	-1.586	61.633	15.811	1.00	45.30
	ATOM	3749	O	ASP A 491	0	-2.809	61.752	15.820	1.00	45.60
35	ATOM	3750	CB	ASP A 491	0	-0.764	61.800	18.170	1.00	44.67
	ATOM	3751	CG	ASP A 491	0	-0.441	61.101	19.475	1.00	45.90
	ATOM	3752	OD1	ASP A 491	0	0.149	61.761	20.364	1.00	46.32
	ATOM	3753	OD2	ASP A 491	0	-0.763	59.911	19.669	1.00	46.04

ATOM 3754 N ASP A 492 0 -0.871 62.107 14.817 1.00 46.75
ATOM 3755 CA ASP A 492 0 -1.323 62.804 13.653 1.00 48.98
ATOM 3756 C ASP A 492 0 -1.702 61.936 12.460 1.00 49.48
ATOM 3757 O ASP A 492 0 -2.002 62.458 11.378 1.00 50.24
5 ATOM 3758 CB ASP A 492 0 -0.155 63.649 13.107 1.00 51.54
ATOM 3759 CG ASP A 492 0 -0.168 65.081 13.587 1.00 53.57
ATOM 3760 OD1 ASP A 492 0 -0.886 65.375 14.570 1.00 54.07
ATOM 3761 OD2 ASP A 492 0 0.576 65.857 12.939 1.00 55.04
ATOM 3762 N LEU A 493 0 -1.554 60.630 12.584 1.00 49.01
10 ATOM 3763 CA LEU A 493 0 -1.896 59.732 11.483 1.00 47.63
ATOM 3764 C LEU A 493 0 -3.377 59.872 11.137 1.00 47.61
ATOM 3765 O LEU A 493 0 -4.209 60.018 12.027 1.00 47.02
ATOM 3766 CB LEU A 493 0 -1.661 58.296 11.940 1.00 46.08
ATOM 3767 CG LEU A 493 0 -0.485 57.463 11.464 1.00 45.24
15 ATOM 3768 CD1 LEU A 493 0 0.616 58.224 10.756 1.00 43.57
ATOM 3769 CD2 LEU A 493 0 0.075 56.710 12.669 1.00 44.62
ATOM 3770 N PRO A 494 0 -3.694 59.763 9.866 1.00 48.01
ATOM 3771 CA PRO A 494 0 -5.049 59.734 9.353 1.00 49.11
ATOM 3772 C PRO A 494 0 -5.617 58.339 9.570 1.00 51.21
20 ATOM 3773 O PRO A 494 0 -4.919 57.325 9.495 1.00 50.61
ATOM 3774 CB PRO A 494 0 -4.938 59.995 7.843 1.00 48.94
ATOM 3775 CG PRO A 494 0 -3.559 59.463 7.544 1.00 48.47
ATOM 3776 CD PRO A 494 0 -2.714 59.538 8.797 1.00 48.22
ATOM 3777 N PRO A 495 0 -6.915 58.238 9.796 1.00 53.24
25 ATOM 3778 CA PRO A 495 0 -7.630 57.006 10.055 1.00 53.93
ATOM 3779 C PRO A 495 0 -7.404 55.890 9.058 1.00 54.84
ATOM 3780 O PRO A 495 0 -7.348 54.705 9.423 1.00 55.08
ATOM 3781 CB PRO A 495 0 -9.126 57.362 10.146 1.00 54.40
ATOM 3782 CG PRO A 495 0 -9.090 58.848 10.391 1.00 54.17
30 ATOM 3783 CD PRO A 495 0 -7.787 59.420 9.895 1.00 53.58
ATOM 3784 N GLU A 496 0 -7.190 56.198 7.784 1.00 55.36
ATOM 3785 CA GLU A 496 0 -6.936 55.187 6.763 1.00 55.83
ATOM 3786 C GLU A 496 0 -5.582 54.521 6.971 1.00 54.09
ATOM 3787 O GLU A 496 0 -5.345 53.406 6.505 1.00 53.29
35 ATOM 3788 CB GLU A 496 0 -7.091 55.805 5.378 1.00 57.96
ATOM 3789 CG GLU A 496 0 -6.030 55.604 4.339 1.00 61.30
ATOM 3790 CD GLU A 496 0 -6.448 54.984 3.025 1.00 63.68
ATOM 3791 OE1 GLU A 496 0 -7.449 55.411 2.388 1.00 65.15

ATOM 3792 OE2 GLU A 496 0 -5.747 54.034 2.586 1.00 64.91
ATOM 3793 N ALA A 497 0 -4.665 55.217 7.630 1.00 52.35
ATOM 3794 CA ALA A 497 0 -3.326 54.738 7.886 1.00 50.83
ATOM 3795 C ALA A 497 0 -3.245 53.626 8.924 1.00 49.08
5 ATOM 3796 O ALA A 497 0 -2.361 52.773 8.794 1.00 47.61
ATOM 3797 CB ALA A 497 0 -2.443 55.910 8.317 1.00 51.23
ATOM 3798 N THR A 498 0 -4.113 53.630 9.926 1.00 48.01
ATOM 3799 CA THR A 498 0 -4.086 52.617 10.964 1.00 48.73
ATOM 3800 C THR A 498 0 -5.271 51.656 10.938 1.00 48.99
10 ATOM 3801 O THR A 498 0 -5.425 50.852 11.862 1.00 47.81
ATOM 3802 CB THR A 498 0 -4.055 53.223 12.388 1.00 49.04
ATOM 3803 OG1 THR A 498 0 -5.315 53.816 12.752 1.00 47.95
ATOM 3804 CG2 THR A 498 0 -2.919 54.223 12.514 1.00 48.94
ATOM 3805 N SER A 499 0 -6.101 51.756 9.911 1.00 49.78
15 ATOM 3806 CA SER A 499 0 -7.307 50.933 9.814 1.00 51.20
ATOM 3807 C SER A 499 0 -7.048 49.470 9.494 1.00 49.98
ATOM 3808 O SER A 499 0 -6.257 49.143 8.617 1.00 48.80
ATOM 3809 CB SER A 499 0 -8.223 51.606 8.800 1.00 52.62
ATOM 3810 OG SER A 499 0 -8.428 50.827 7.596 1.00 55.22
20 ATOM 3811 N ILE A 500 0 -7.706 48.585 10.230 1.00 50.08
ATOM 3812 CA ILE A 500 0 -7.563 47.151 10.077 1.00 51.25
ATOM 3813 C ILE A 500 0 -8.642 46.518 9.207 1.00 53.08
ATOM 3814 O ILE A 500 0 -9.785 46.351 9.639 1.00 54.00
ATOM 3815 CB ILE A 500 0 -7.631 46.428 11.436 1.00 50.61
25 ATOM 3816 CG1 ILE A 500 0 -6.475 46.866 12.336 1.00 50.22
ATOM 3817 CG2 ILE A 500 0 -7.619 44.907 11.302 1.00 50.34
ATOM 3818 CD1 ILE A 500 0 -6.806 46.617 13.800 1.00 50.52
ATOM 3819 N GLN A 501 0 -8.263 46.074 8.024 1.00 54.35
ATOM 3820 CA GLN A 501 0 -9.177 45.360 7.129 1.00 55.14
30 ATOM 3821 C GLN A 501 0 -9.298 43.904 7.564 1.00 55.85
ATOM 3822 O GLN A 501 0 -8.335 43.130 7.556 1.00 55.59
ATOM 3823 CB GLN A 501 0 -8.594 45.485 5.732 1.00 55.56
ATOM 3824 CG GLN A 501 0 -9.262 44.736 4.604 1.00 56.32
ATOM 3825 CD GLN A 501 0 -8.874 45.369 3.271 1.00 57.46
35 ATOM 3826 OE1 GLN A 501 0 -8.480 44.667 2.336 1.00 57.35
ATOM 3827 NE2 GLN A 501 0 -8.998 46.697 3.219 1.00 57.61
ATOM 3828 N THR A 502 0 -10.493 43.506 7.968 1.00 57.08
ATOM 3829 CA THR A 502 0 -10.788 42.146 8.401 1.00 58.28

ATOM 3830 C THR A 502 O -10.966 41.205 7.216 1.00 58.80
ATOM 3831 O THR A 502 O -11.199 41.604 6.074 1.00 58.71
ATOM 3832 CB THR A 502 O -12.046 42.108 9.293 1.00 58.99
ATOM 3833 OG1 THR A 502 O -11.794 42.909 10.464 1.00 59.62
5 ATOM 3834 CG2 THR A 502 O -12.421 40.707 9.749 1.00 58.74
ATOM 3835 N VAL A 503 O -10.746 39.922 7.471 1.00 59.20
ATOM 3836 CA VAL A 503 O -10.904 38.877 6.468 1.00 60.27
ATOM 3837 C VAL A 503 O -11.687 37.736 7.119 1.00 61.11
ATOM 3838 O VAL A 503 O -11.606 37.563 8.341 1.00 61.03
10 ATOM 3839 CB VAL A 503 O -9.589 38.430 5.823 1.00 59.97
ATOM 3840 CG1 VAL A 503 O -8.337 38.964 6.507 1.00 59.65
ATOM 3841 CG2 VAL A 503 O -9.467 36.914 5.722 1.00 59.97
ATOM 3842 N VAL A 504 O -12.478 37.002 6.341 1.00 61.77
ATOM 3843 CA VAL A 504 O -13.203 35.863 6.911 1.00 62.40
15 ATOM 3844 C VAL A 504 O -12.673 34.579 6.259 1.00 62.99
ATOM 3845 O VAL A 504 O -11.811 33.894 6.803 1.00 63.13
ATOM 3846 CB VAL A 504 O -14.730 35.882 6.756 1.00 62.39
ATOM 3847 CG1 VAL A 504 O -15.392 36.931 7.635 1.00 61.89
ATOM 3848 CG2 VAL A 504 O -15.127 36.068 5.297 1.00 62.17
20 ATOM 3849 C1 NAG A 800 O -2.401 42.835 45.802 1.00 30.44
ATOM 3850 C2 NAG A 800 O -1.327 43.232 46.780 1.00 31.80
ATOM 3851 N2 NAG A 800 O -0.119 43.561 45.983 1.00 31.37
ATOM 3852 C7 NAG A 800 O 0.179 44.844 45.683 1.00 32.37
ATOM 3853 O7 NAG A 800 O -0.549 45.688 45.982 1.00 34.61
25 ATOM 3854 C8 NAG A 800 O 1.457 45.094 44.983 1.00 31.67
ATOM 3855 C3 NAG A 800 O -1.015 42.187 47.801 1.00 32.94
ATOM 3856 O3 NAG A 800 O -0.264 42.838 48.796 1.00 34.46
ATOM 3857 C4 NAG A 800 O -2.351 41.662 48.377 1.00 34.05
ATOM 3858 O4 NAG A 800 O -2.097 40.644 49.344 1.00 35.62
30 ATOM 3859 C5 NAG A 800 O -3.128 41.025 47.202 1.00 35.11
ATOM 3860 O5 NAG A 800 O -3.466 42.046 46.295 1.00 33.06
ATOM 3861 C6 NAG A 800 O -4.444 40.420 47.673 1.00 36.66
ATOM 3862 O6 NAG A 800 O -5.199 41.411 48.288 1.00 39.73
ATOM 3863 C1 GLC A 900 O -8.957 50.280 6.333 1.00 58.53
35 ATOM 3864 C2 GLC A 900 O -8.500 49.605 5.037 1.00 59.25
ATOM 3865 C3 GLC A 900 O -7.806 50.686 4.219 1.00 59.71
ATOM 3866 C4 GLC A 900 O -8.691 51.905 3.987 1.00 60.13
ATOM 3867 C5 GLC A 900 O -9.595 52.289 5.142 1.00 59.22

ATOM 3868 O5 GLC A 900 0 -10.004 51.177 5.937 1.00 59.71
ATOM 3869 CU IUM B 1 0 -1.332 34.401 30.132 1.00 29.47
ATOM 3870 CU IUM B 2 0 7.297 42.245 26.618 1.00 27.01
ATOM 3871 CU IUM B 3 0 9.569 38.786 23.923 1.00 21.38
5 ATOM 3872 O IUM B 5 0 7.445 40.703 25.162 1.00 26.99
ATOM 3873 OW0 WAT W 1 0 19.509 36.893 30.054 1.00 13.07
ATOM 3874 OW0 WAT W 2 0 24.726 29.672 16.651 1.00 7.67
ATOM 3875 OW0 WAT W 3 0 15.295 17.988 35.061 1.00 8.65
ATOM 3876 OW0 WAT W 4 0 6.481 28.311 23.427 1.00 8.00
10 ATOM 3877 OW0 WAT W 5 0 14.921 45.178 24.306 1.00 17.04
ATOM 3878 OW0 WAT W 6 0 14.413 44.401 28.162 1.00 10.12
ATOM 3879 OW0 WAT W 7 0 9.967 21.576 9.620 1.00 11.43
ATOM 3880 OW0 WAT W 8 0 10.088 28.675 13.038 1.00 9.27
ATOM 3881 OW0 WAT W 9 0 9.808 47.902 28.959 1.00 12.71
15 ATOM 3882 OW0 WAT W 10 0 21.976 23.052 35.604 1.00 11.72
ATOM 3883 OW0 WAT W 11 0 10.862 25.744 29.928 1.00 10.21
ATOM 3884 OW0 WAT W 12 0 26.087 32.996 23.097 1.00 14.21
ATOM 3885 OW0 WAT W 13 0 22.256 58.745 37.931 1.00 17.85
ATOM 3886 OW0 WAT W 14 0 -0.104 29.831 35.249 1.00 16.36
20 ATOM 3887 OW0 WAT W 15 0 18.153 61.857 36.641 1.00 14.38
ATOM 3888 OW0 WAT W 16 0 9.426 38.431 9.161 1.00 15.35
ATOM 3889 OW0 WAT W 17 0 7.639 24.371 3.713 1.00 22.18
ATOM 3890 OW0 WAT W 18 0 27.977 11.643 9.481 1.00 19.22
ATOM 3891 OW0 WAT W 19 0 3.140 21.028 24.695 1.00 11.12
25 ATOM 3892 OW0 WAT W 20 0 9.847 20.701 30.902 1.00 16.16
ATOM 3893 OW0 WAT W 21 0 -1.517 29.009 43.180 1.00 27.18
ATOM 3894 OW0 WAT W 22 0 3.497 29.138 26.088 1.00 17.22
ATOM 3895 OW0 WAT W 23 0 20.614 32.765 40.433 1.00 17.63
ATOM 3896 OW0 WAT W 24 0 19.098 51.778 39.452 1.00 22.33
30 ATOM 3897 OW0 WAT W 25 0 0.977 21.396 5.064 1.00 18.54
ATOM 3898 OW0 WAT W 26 0 8.546 16.150 21.761 1.00 16.40
ATOM 3899 OW0 WAT W 27 0 6.102 19.858 10.350 1.00 17.79
ATOM 3900 OW0 WAT W 28 0 11.702 55.189 41.955 1.00 18.92
ATOM 3901 OW0 WAT W 29 0 3.360 42.251 18.209 1.00 16.26
35 ATOM 3902 OW0 WAT W 30 0 6.232 14.672 22.473 1.00 24.49
ATOM 3903 OW0 WAT W 31 0 16.729 26.542 39.731 1.00 15.28
ATOM 3904 OW0 WAT W 32 0 2.834 30.640 40.601 1.00 18.11
ATOM 3905 OW0 WAT W 33 0 21.893 42.837 27.884 1.00 15.08

	ATOM	3906	OW0	WAT	W	34	0	1.581	28.193	27.914	1.00	17.77
	ATOM	3907	OW0	WAT	W	35	0	-3.503	21.749	11.578	1.00	15.32
	ATOM	3908	OW0	WAT	W	36	0	7.131	33.344	11.786	1.00	18.18
	ATOM	3909	OW0	WAT	W	37	0	17.312	38.603	29.961	1.00	14.75
5	ATOM	3910	OW0	WAT	W	38	0	-6.705	40.723	39.909	1.00	23.49
	ATOM	3911	OW0	WAT	W	39	0	9.010	31.121	11.736	1.00	19.99
	ATOM	3912	OW0	WAT	W	40	0	9.376	28.353	33.076	1.00	16.22
	ATOM	3913	OW0	WAT	W	41	0	30.104	29.895	20.857	1.00	25.77
	ATOM	3914	OW0	WAT	W	42	0	-6.950	33.663	21.335	1.00	26.62
10	ATOM	3915	OW0	WAT	W	43	0	8.541	27.867	36.827	1.00	12.80
	ATOM	3916	OW0	WAT	W	44	0	3.590	21.651	11.893	1.00	14.46
	ATOM	3917	OW0	WAT	W	45	0	23.290	21.665	37.787	1.00	28.75
	ATOM	3918	OW0	WAT	W	46	0	22.724	11.873	22.270	1.00	23.07
	ATOM	3919	OW0	WAT	W	47	0	-1.090	42.001	12.877	1.00	19.33
15	ATOM	3920	OW0	WAT	W	48	0	14.091	27.298	40.583	1.00	18.51
	ATOM	3921	OW0	WAT	W	49	0	2.336	52.026	29.983	1.00	25.66
	ATOM	3922	OW0	WAT	W	50	0	15.475	14.450	22.853	1.00	20.37
	ATOM	3923	OW0	WAT	W	51	0	25.945	26.568	40.287	1.00	24.49
	ATOM	3924	OW0	WAT	W	52	0	19.545	41.598	35.087	1.00	20.70
20	ATOM	3925	OW0	WAT	W	53	0	-3.802	47.942	9.638	1.00	29.98
	ATOM	3926	OW0	WAT	W	54	0	-7.478	41.160	9.585	1.00	24.26
	ATOM	3927	OW0	WAT	W	55	0	-2.938	29.733	36.048	1.00	22.93
	ATOM	3928	OW0	WAT	W	56	0	29.051	32.114	22.680	1.00	22.50
	ATOM	3929	OW0	WAT	W	57	0	0.360	29.505	5.595	1.00	17.78
25	ATOM	3930	OW0	WAT	W	58	0	8.583	57.422	21.440	1.00	21.90
	ATOM	3931	OW0	WAT	W	59	0	25.151	31.947	34.812	1.00	22.13
	ATOM	3932	OW0	WAT	W	60	0	25.133	62.204	32.968	1.00	25.75
	ATOM	3933	OW0	WAT	W	61	0	14.909	40.770	30.294	1.00	17.25
	ATOM	3934	OW0	WAT	W	62	0	20.825	30.520	34.676	1.00	16.18
30	ATOM	3935	OW0	WAT	W	63	0	5.509	26.744	43.167	1.00	30.12
	ATOM	3936	OW0	WAT	W	64	0	5.280	57.279	14.627	1.00	22.66
	ATOM	3937	OW0	WAT	W	65	0	2.944	53.436	32.359	1.00	22.97
	ATOM	3938	OW0	WAT	W	66	0	11.266	43.508	3.407	1.00	20.01
	ATOM	3939	OW0	WAT	W	67	0	21.535	45.549	26.563	1.00	24.47
35	ATOM	3940	OW0	WAT	W	68	0	0.412	33.358	11.837	1.00	19.89
	ATOM	3941	OW0	WAT	W	69	0	26.466	32.305	25.785	1.00	20.19
	ATOM	3942	OW0	WAT	W	70	0	0.910	45.068	7.829	1.00	22.05
	ATOM	3943	OW0	WAT	W	71	0	-2.060	46.506	39.381	1.00	23.49

	ATOM	3944	OW0	WAT	W	72	0	20.236	56.718	25.851	1.00	23.74
	ATOM	3945	OW0	WAT	W	73	0	3.253	23.017	38.254	1.00	24.83
	ATOM	3946	OW0	WAT	W	74	0	9.653	22.835	35.143	1.00	25.79
	ATOM	3947	OW0	WAT	W	75	0	16.877	52.904	47.331	1.00	24.42
5	ATOM	3948	OW0	WAT	W	76	0	14.293	22.021	3.993	1.00	32.28
	ATOM	3949	OW0	WAT	W	77	0	-5.287	19.835	18.528	1.00	24.65
	ATOM	3950	OW0	WAT	W	78	0	8.414	38.317	49.069	1.00	28.77
	ATOM	3951	OW0	WAT	W	79	0	7.070	32.466	47.926	1.00	21.83
	ATOM	3952	OW0	WAT	W	80	0	-0.452	28.307	25.779	1.00	16.58
10	ATOM	3953	OW0	WAT	W	81	0	14.774	15.006	34.455	1.00	25.63
	ATOM	3954	OW0	WAT	W	82	0	11.515	54.942	35.962	1.00	14.20
	ATOM	3955	OW0	WAT	W	83	0	25.643	33.451	32.105	1.00	30.31
	ATOM	3956	OW0	WAT	W	84	0	11.869	12.221	20.394	1.00	31.37
	ATOM	3957	OW0	WAT	W	85	0	11.653	51.587	22.411	1.00	16.48
15	ATOM	3958	OW0	WAT	W	86	0	17.334	40.837	51.079	1.00	30.26
	ATOM	3959	OW0	WAT	W	87	0	4.355	25.208	34.030	1.00	32.26
	ATOM	3960	OW0	WAT	W	88	0	18.816	52.360	32.512	1.00	21.19
	ATOM	3961	OW0	WAT	W	89	0	-2.704	46.518	35.364	1.00	21.99
	ATOM	3962	OW0	WAT	W	90	0	18.793	27.893	49.481	1.00	24.52
20	ATOM	3963	OW0	WAT	W	91	0	22.459	46.584	28.898	1.00	18.99
	ATOM	3964	OW0	WAT	W	92	0	7.958	34.422	49.370	1.00	26.14
	ATOM	3965	OW0	WAT	W	93	0	23.972	16.246	6.806	1.00	24.35
	ATOM	3966	OW0	WAT	W	94	0	1.340	49.185	26.307	1.00	31.64
	ATOM	3967	OW0	WAT	W	95	0	-1.830	35.291	12.266	1.00	27.28
25	ATOM	3968	OW0	WAT	W	96	0	20.460	17.486	3.589	1.00	33.51
	ATOM	3969	OW0	WAT	W	97	0	15.177	6.964	9.868	1.00	24.40
	ATOM	3970	OW0	WAT	W	98	0	18.616	57.927	43.922	1.00	30.76
	ATOM	3971	OW0	WAT	W	99	0	10.562	32.112	9.972	1.00	28.90
	ATOM	3972	OW0	WAT	W	100	0	1.630	61.363	10.878	1.00	33.92
30	ATOM	3973	OW0	WAT	W	101	0	-4.939	49.989	33.211	1.00	29.73
	ATOM	3974	OW0	WAT	W	102	0	19.385	44.813	34.546	1.00	23.52
	ATOM	3975	OW0	WAT	W	103	0	19.055	43.063	37.581	1.00	30.59
	ATOM	3976	OW0	WAT	W	105	0	28.703	33.555	27.406	1.00	32.92
	ATOM	3977	OW0	WAT	W	106	0	28.835	19.646	10.759	1.00	40.44
35	ATOM	3978	OW0	WAT	W	107	0	22.047	22.465	9.758	1.00	29.98
	ATOM	3979	OW0	WAT	W	108	0	14.689	61.032	36.346	1.00	30.63
	ATOM	3980	OW0	WAT	W	109	0	16.998	24.042	9.318	1.00	23.90
	ATOM	3981	OW0	WAT	W	110	0	13.472	30.533	11.848	1.00	34.83

	ATOM	3982	OW0	WAT	W	111	0	-2.175	35.601	41.496	1.00	28.55
	ATOM	3983	OW0	WAT	W	112	0	1.528	17.373	-1.396	1.00	38.21
	ATOM	3984	OW0	WAT	W	113	0	-2.856	29.748	19.681	1.00	30.55
	ATOM	3985	OW0	WAT	W	114	0	2.377	42.810	47.971	1.00	26.87
5	ATOM	3986	OW0	WAT	W	115	0	10.947	12.820	33.745	1.00	31.60
	ATOM	3987	OW0	WAT	W	116	0	9.807	58.194	12.442	1.00	29.63
	ATOM	3988	OW0	WAT	W	117	0	18.488	62.559	29.470	1.00	45.83
	ATOM	3989	OW0	WAT	W	118	0	11.708	61.566	40.940	1.00	37.19
	ATOM	3990	OW0	WAT	W	119	0	-10.101	22.257	15.091	1.00	30.48
10	ATOM	3991	OW0	WAT	W	120	0	-1.930	15.913	7.386	1.00	36.63
	ATOM	3992	OW0	WAT	W	121	0	23.988	43.686	29.319	1.00	32.15
	ATOM	3993	OW0	WAT	W	122	0	7.354	57.153	12.809	1.00	28.10
	ATOM	3994	OW0	WAT	W	123	0	24.207	22.101	11.958	1.00	32.83
	ATOM	3995	OW0	WAT	W	124	0	-1.268	15.083	9.738	1.00	32.53
15	ATOM	3996	OW0	WAT	W	125	0	19.363	5.047	13.812	1.00	34.57
	ATOM	3997	OW0	WAT	W	126	0	4.799	41.145	23.688	1.00	28.33
	ATOM	3998	OW0	WAT	W	127	0	15.975	23.287	5.889	1.00	30.95
	ATOM	3999	OW0	WAT	W	128	0	3.698	38.582	-2.369	1.00	36.84
	ATOM	4000	OW0	WAT	W	129	0	-2.601	49.124	11.710	1.00	28.91
20	ATOM	4001	OW0	WAT	W	130	0	15.779	56.598	43.285	1.00	27.76
	ATOM	4002	OW0	WAT	W	131	0	26.306	32.724	13.233	1.00	37.94
	ATOM	4003	OW0	WAT	W	132	0	3.610	46.947	23.991	1.00	35.49
	ATOM	4004	OW0	WAT	W	133	0	18.354	11.929	29.348	1.00	33.88
	ATOM	4005	OW0	WAT	W	134	0	13.966	41.517	27.765	1.00	18.02
25	ATOM	4006	OW0	WAT	W	135	0	23.545	49.080	27.785	1.00	25.21
	ATOM	4007	OW0	WAT	W	136	0	16.876	25.082	41.791	1.00	28.71
	ATOM	4008	OW0	WAT	W	137	0	15.439	54.809	45.527	1.00	35.30
	ATOM	4009	OW0	WAT	W	138	0	11.733	25.676	43.264	1.00	38.24
	ATOM	4010	OW0	WAT	W	139	0	9.795	34.460	11.898	1.00	31.61
30	ATOM	4011	OW0	WAT	W	140	0	13.328	57.569	42.356	1.00	30.66
	ATOM	4012	OW0	WAT	W	141	0	14.146	7.869	20.604	1.00	35.72
	ATOM	4013	OW0	WAT	W	142	0	23.330	12.948	3.922	1.00	29.83
	ATOM	4014	OW0	WAT	W	143	0	16.607	10.575	24.347	1.00	36.47
	ATOM	4015	OW0	WAT	W	144	0	8.509	25.546	35.012	1.00	35.43
35	ATOM	4016	OW0	WAT	W	145	0	12.597	44.457	1.450	1.00	39.54
	ATOM	4017	OW0	WAT	W	146	0	21.680	51.509	39.154	1.00	40.08
	ATOM	4018	OW0	WAT	W	147	0	-0.702	52.593	39.700	1.00	29.62
	ATOM	4019	OW0	WAT	W	148	0	23.269	14.719	22.589	1.00	30.24

	ATOM	4020	OW0	WAT	W	149	0	27.149	22.972	41.846	1.00	35.00
	ATOM	4021	OW0	WAT	W	150	0	2.854	9.792	8.923	1.00	46.35
	ATOM	4022	OW0	WAT	W	151	0	24.831	15.672	24.889	1.00	29.22
	ATOM	4023	OW0	WAT	W	152	0	24.965	51.606	19.113	1.00	32.19
5	ATOM	4024	OW0	WAT	W	153	0	-4.611	25.034	37.817	1.00	46.51
	ATOM	4025	OW0	WAT	W	154	0	12.225	39.382	28.864	1.00	25.42
	ATOM	4026	OW0	WAT	W	155	0	18.332	22.341	43.180	1.00	36.18
	ATOM	4027	OW0	WAT	W	156	0	36.467	20.701	17.144	1.00	44.13
	ATOM	4028	OW0	WAT	W	157	0	-4.903	47.901	40.886	1.00	33.97
10	ATOM	4029	OW0	WAT	W	158	0	12.979	13.955	3.208	1.00	33.60
	ATOM	4030	OW0	WAT	W	159	0	32.383	12.693	24.743	1.00	30.25
	ATOM	4031	OW0	WAT	W	160	0	30.796	26.296	14.368	1.00	44.37
	ATOM	4032	OW0	WAT	W	161	0	19.332	37.280	40.057	1.00	31.54
	ATOM	4033	OW0	WAT	W	162	0	17.625	20.028	41.642	1.00	45.88
15	ATOM	4034	OW0	WAT	W	163	0	19.917	56.115	46.103	1.00	40.37
	ATOM	4035	OW0	WAT	W	164	0	-4.743	14.204	16.748	1.00	40.86
	ATOM	4036	OW0	WAT	W	165	0	0.738	46.912	21.790	1.00	38.56
	ATOM	4037	OW0	WAT	W	166	0	22.648	62.277	30.976	1.00	24.37
	ATOM	4038	OW0	WAT	W	167	0	-4.322	45.754	26.894	1.00	48.97
20	ATOM	4039	OW0	WAT	W	168	0	-2.386	24.601	0.665	1.00	32.57
	ATOM	4040	OW0	WAT	W	169	0	-0.459	41.618	35.838	1.00	35.25
	ATOM	4041	OW0	WAT	W	170	0	26.659	4.722	11.434	1.00	41.25
	ATOM	4042	OW0	WAT	W	171	0	13.720	11.379	22.121	1.00	39.59
	ATOM	4043	OW0	WAT	W	172	0	15.266	7.451	6.576	1.00	41.71
25	ATOM	4044	OW0	WAT	W	173	0	0.134	17.450	6.165	1.00	42.12
	ATOM	4045	OW0	WAT	W	174	0	38.646	32.884	25.247	1.00	41.80
	ATOM	4046	OW0	WAT	W	175	0	10.591	17.398	3.251	1.00	29.37
	ATOM	4047	OW0	WAT	W	176	0	22.444	49.424	25.264	1.00	19.51
	ATOM	4048	OW0	WAT	W	177	0	0.429	23.224	28.598	1.00	33.54
30	ATOM	4049	OW0	WAT	W	178	0	-2.302	27.278	34.780	1.00	44.76
	ATOM	4050	OW0	WAT	W	179	0	2.054	25.866	16.462	1.00	34.29
	ATOM	4051	OW0	WAT	W	180	0	30.277	18.006	25.789	1.00	42.28
	ATOM	4052	OW0	WAT	W	181	0	2.316	18.424	27.884	1.00	47.39
	ATOM	4053	OW0	WAT	W	182	0	19.401	41.164	39.560	1.00	39.68
35	ATOM	4054	OW0	WAT	W	183	0	23.742	10.982	24.879	1.00	43.32
	ATOM	4055	OW0	WAT	W	184	0	3.926	24.450	44.251	1.00	48.95
	ATOM	4056	OW0	WAT	W	185	0	25.186	21.211	40.951	1.00	39.05
	ATOM	4057	OW0	WAT	W	186	0	20.353	34.816	48.799	1.00	34.08

	ATOM	4058	OW0	WAT	W	187	0	35.782	22.476	21.693	1.00	40.04
	ATOM	4059	OW0	WAT	W	188	0	27.256	23.617	12.235	1.00	40.85
	ATOM	4060	OW0	WAT	W	189	0	6.777	12.502	12.641	1.00	53.37
	ATOM	4061	OW0	WAT	W	190	0	-4.663	38.998	4.159	1.00	39.85
5	ATOM	4062	OW0	WAT	W	191	0	24.398	52.064	24.607	1.00	45.51
	ATOM	4063	OW0	WAT	W	192	0	1.808	15.541	4.832	1.00	41.06
	ATOM	4064	OW0	WAT	W	193	0	5.341	36.359	7.569	1.00	39.36
	ATOM	4065	OW0	WAT	W	194	0	32.192	38.650	21.799	1.00	37.18
	ATOM	4066	OW0	WAT	W	195	0	-10.782	36.616	38.705	1.00	50.35
10	ATOM	4067	OW0	WAT	W	196	0	4.119	64.116	32.946	1.00	34.51
	ATOM	4068	OW0	WAT	W	197	0	19.427	22.772	5.898	1.00	37.94
	ATOM	4069	OW0	WAT	W	198	0	-4.671	33.476	1.652	1.00	43.38
	ATOM	4070	OW0	WAT	W	199	0	-8.983	23.757	17.693	1.00	57.10
	ATOM	4071	OW0	WAT	W	200	0	-6.735	22.473	20.432	1.00	38.49
15	ATOM	4072	OW0	WAT	W	201	0	-6.954	26.746	37.309	1.00	55.48
	ATOM	4073	OW0	WAT	W	202	0	23.418	38.662	33.700	1.00	42.20
	ATOM	4074	OW0	WAT	W	203	0	9.004	24.070	36.971	1.00	40.06
	ATOM	4075	OW0	WAT	W	204	0	18.890	42.920	51.502	1.00	46.29
	ATOM	4076	OW0	WAT	W	205	0	13.301	18.514	3.624	1.00	42.17
20	ATOM	4077	OW0	WAT	W	206	0	31.189	12.995	19.645	1.00	51.92
	ATOM	4078	OW0	WAT	W	207	0	15.589	57.456	13.738	1.00	38.96
	ATOM	4079	OW0	WAT	W	208	0	-3.389	12.961	12.738	1.00	46.99
	ATOM	4080	OW0	WAT	W	209	0	9.321	30.475	6.320	1.00	49.75
	ATOM	4081	OW0	WAT	W	210	0	1.680	61.379	33.738	1.00	37.48
25	ATOM	4082	OW0	WAT	W	211	0	-3.811	36.417	3.807	1.00	46.01
	ATOM	4083	OW0	WAT	W	212	0	17.087	46.902	3.830	1.00	45.12
	ATOM	4084	OW0	WAT	W	213	0	23.702	22.325	43.022	1.00	36.14
	ATOM	4085	OW0	WAT	W	214	0	10.849	60.003	14.389	1.00	32.05
	ATOM	4086	OW0	WAT	W	215	0	34.001	25.493	20.855	1.00	40.75
30	ATOM	4087	OW0	WAT	W	216	0	27.422	37.093	28.951	1.00	42.33
	ATOM	4088	OW0	WAT	W	217	0	2.471	63.256	35.173	1.00	48.36
	ATOM	4089	OW0	WAT	W	218	0	-0.973	59.086	28.720	1.00	53.14
	ATOM	4090	OW0	WAT	W	219	0	28.841	9.287	6.463	1.00	39.02
	ATOM	4091	OW0	WAT	W	220	0	-5.593	21.802	9.619	1.00	44.21
35	ATOM	4092	OW0	WAT	W	221	0	22.109	15.521	1.696	1.00	38.33
	ATOM	4093	OW0	WAT	W	222	0	13.029	32.860	12.233	1.00	37.63
	ATOM	4094	OW0	WAT	W	223	0	11.840	33.823	3.800	1.00	42.20
	ATOM	4095	OW0	WAT	W	224	0	8.476	42.976	-0.104	1.00	40.23

	ATOM	4096	OW0	WAT	W	225	0	6.607	9.754	13.906	1.00	41.30
	ATOM	4097	OW0	WAT	W	226	0	22.513	32.613	49.067	1.00	47.26
	ATOM	4098	OW0	WAT	W	227	0	13.790	4.924	16.718	1.00	38.05
	ATOM	4099	OW0	WAT	W	228	0	4.578	46.381	2.146	1.00	38.90
5	ATOM	4100	OW0	WAT	W	229	0	-0.178	18.054	23.533	1.00	43.42
	ATOM	4101	OW0	WAT	W	230	0	-5.146	34.010	4.766	1.00	38.90
	ATOM	4102	OW0	WAT	W	231	0	20.232	28.890	51.507	1.00	44.95
	ATOM	4103	OW0	WAT	W	232	0	16.083	32.879	10.309	1.00	45.29
	ATOM	4104	OW0	WAT	W	233	0	22.111	51.333	10.599	1.00	34.03
10	ATOM	4105	OW0	WAT	W	234	0	3.247	15.790	28.046	1.00	50.25
	ATOM	4106	OW0	WAT	W	235	0	5.547	11.598	9.674	1.00	56.39
	ATOM	4107	OW0	WAT	W	236	0	-1.085	18.297	-2.265	1.00	45.26
	ATOM	4108	OW0	WAT	W	237	0	30.994	12.013	22.690	1.00	50.37
	ATOM	4109	OW0	WAT	W	238	0	24.691	33.260	27.819	1.00	37.65
15	ATOM	4110	OW0	WAT	W	239	0	18.911	40.770	5.815	1.00	44.15
	ATOM	4111	OW0	WAT	W	240	0	21.532	53.033	33.280	1.00	31.23
	ATOM	4112	OW0	WAT	W	241	0	19.745	46.029	4.364	1.00	46.38
	ATOM	4113	OW0	WAT	W	242	0	27.516	16.526	25.474	1.00	51.75
	ATOM	4114	OW0	WAT	W	243	0	34.171	19.604	8.423	1.00	55.79
20	ATOM	4115	OW0	WAT	W	244	0	23.870	53.512	11.474	1.00	42.01
	ATOM	4116	OW0	WAT	W	245	0	14.492	23.842	44.882	1.00	52.25
	ATOM	4117	OW0	WAT	W	246	0	-3.070	63.260	33.189	1.00	40.77
	ATOM	4118	OW0	WAT	W	247	0	22.185	55.701	37.353	1.00	39.52
	ATOM	4119	OW0	WAT	W	248	0	14.144	26.239	42.825	1.00	42.50
25	ATOM	4120	OW0	WAT	W	249	0	25.026	36.545	35.213	1.00	58.19
	ATOM	4121	OW0	WAT	W	250	0	27.072	34.293	43.895	1.00	46.58
	ATOM	4122	OW0	WAT	W	251	0	11.742	7.192	4.856	1.00	42.78
	ATOM	4123	OW0	WAT	W	252	0	0.730	46.405	24.947	1.00	39.31
	ATOM	4124	OW0	WAT	W	253	0	28.346	34.036	30.808	1.00	43.10
30	ATOM	4125	OW0	WAT	W	254	0	-3.838	40.281	1.903	1.00	38.67
	ATOM	4126	OW0	WAT	W	255	0	6.837	35.163	51.935	1.00	58.57
	ATOM	4127	OW0	WAT	W	256	0	19.740	62.853	17.880	1.00	52.39
	ATOM	4128	OW0	WAT	W	258	0	-0.994	41.755	22.088	0.00	69.57
	ATOM	4129	OW0	WAT	W	259	0	1.221	10.473	15.458	1.00	54.80
35	ATOM	4130	OW0	WAT	W	260	0	23.445	55.367	31.430	1.00	48.90
	ATOM	4131	OW0	WAT	W	261	0	23.757	57.854	34.657	1.00	37.69
	ATOM	4132	OW0	WAT	W	262	0	8.508	19.111	34.572	1.00	55.52
	ATOM	4133	OW0	WAT	W	263	0	22.806	22.381	3.611	1.00	64.20

	ATOM	4134	OW0	WAT	W	264	0	0.398	22.602	42.625	1.00	58.86
	ATOM	4135	OW0	WAT	W	265	0	4.195	52.287	43.465	1.00	36.84
	ATOM	4136	OW0	WAT	W	266	0	20.211	6.536	4.911	1.00	39.34
	ATOM	4137	OW0	WAT	W	267	0	14.680	16.117	2.803	1.00	45.76
5	ATOM	4138	OW0	WAT	W	268	0	14.938	25.582	6.850	1.00	41.01
	ATOM	4139	OW0	WAT	W	269	0	7.763	7.940	31.891	0.00	71.30
	ATOM	4140	OW0	WAT	W	270	0	-3.459	33.491	39.400	1.00	40.80
	ATOM	4141	OW0	WAT	W	271	0	23.154	22.897	6.985	1.00	48.25
	ATOM	4142	OW0	WAT	W	272	0	34.916	25.555	28.092	1.00	52.63
10	ATOM	4143	OW0	WAT	W	273	0	8.332	45.481	50.776	1.00	47.23
	ATOM	4144	OW0	WAT	W	274	0	-3.441	57.643	28.775	1.00	49.70
	ATOM	4145	OW0	WAT	W	275	0	23.213	40.573	47.561	1.00	56.02
	ATOM	4146	OW0	WAT	W	276	0	5.421	55.179	45.172	1.00	52.70
	ATOM	4147	OW0	WAT	W	277	0	-3.012	21.908	40.933	1.00	41.69
15	ATOM	4148	OW0	WAT	W	278	0	26.328	53.637	17.905	1.00	37.80
	ATOM	4149	OW0	WAT	W	279	0	9.740	58.922	43.485	1.00	52.06
	ATOM	4150	OW0	WAT	W	280	0	23.545	15.660	4.258	1.00	41.55
	ATOM	4151	OW0	WAT	W	281	0	22.652	31.154	51.246	1.00	58.65
	ATOM	4152	OW0	WAT	W	282	0	22.192	51.135	8.251	1.00	44.76
20	ATOM	4153	OW0	WAT	W	283	0	-6.046	22.886	24.288	1.00	52.40
	ATOM	4154	OW0	WAT	W	284	0	19.949	45.276	49.516	1.00	54.58
	ATOM	4155	OW0	WAT	W	285	0	7.388	22.308	32.108	1.00	43.62
	ATOM	4156	OW0	WAT	W	286	0	15.080	50.452	2.795	1.00	52.20
	ATOM	4157	OW0	WAT	W	287	0	1.016	62.235	30.878	1.00	56.81
25	ATOM	4158	OW0	WAT	W	288	0	23.803	52.570	27.699	1.00	56.22
	ATOM	4159	OW0	WAT	W	289	0	-10.525	31.623	13.870	1.00	47.21
	ATOM	4160	OW0	WAT	W	290	0	1.599	55.502	24.567	1.00	44.50
	ATOM	4161	OW0	WAT	W	291	0	-15.671	37.251	14.660	1.00	83.62
	ATOM	4162	OW0	WAT	W	292	0	7.231	7.950	17.754	1.00	50.61
30	ATOM	4163	OW0	WAT	W	293	0	-4.009	34.057	42.492	1.00	78.48
	ATOM	4164	OW0	WAT	W	294	0	21.004	58.371	18.690	1.00	61.15
	ATOM	4165	OW0	WAT	W	295	0	16.405	48.869	52.211	1.00	53.17
	ATOM	4166	OW0	WAT	W	296	0	7.329	31.202	1.964	1.00	38.86
	ATOM	4167	OW0	WAT	W	297	0	9.518	53.886	5.467	1.00	41.62
35	ATOM	4168	OW0	WAT	W	298	0	10.398	48.995	0.335	1.00	49.64
	ATOM	4169	OW0	WAT	W	299	0	9.889	15.077	3.774	1.00	42.28
	ATOM	4170	OW0	WAT	W	300	0	15.854	56.731	10.934	1.00	44.02

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT:

(A) NAME: NOVO NORDISK
 (B) STREET: Novo Alle
 (C) CITY: Bagsvaerd
 (E) COUNTRY: Denmark
 (F) POSTAL CODE (ZIP): DK-2800
 (G) TELEPHONE: +45 44 44 88 88
 (H) TELEFAX: +45 44 49 05 55

15 (ii) TITLE OF INVENTION: LACCASE MUTANTS

(iii) NUMBER OF SEQUENCES: 10

20 (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 539 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Phe Lys Asn Leu Leu Ser Phe Ala Leu Leu Ala Ile Ser Val Ala
 1 5 10 15
 Asn Ala Gln Ile Val Asn Ser Val Asp Thr Met Thr Leu Thr Asn Ala
 20 25 30
 Asn Val Ser Pro Asp Gly Phe Thr Arg Ala Gly Ile Leu Val Asn Gly
 35 40 45
 Val His Gly Pro Leu Ile Arg Gly Gly Lys Asn Asp Asn Phe Glu Leu
 50 55 60
 Asn Val Val Asn Asp Leu Asp Asn Pro Thr Met Leu Arg Pro Thr Ser
 65 70 75 80
 Ile His Trp His Gly Leu Phe Gln Arg Gly Thr Asn Trp Ala Asp Gly
 85 90 95
 Ala Asp Gly Val Asn Gln Cys Pro Ile Ser Pro Gly His Ala Phe Leu
 100 105 110
 Tyr Lys Phe Thr Pro Ala Gly His Ala Gly Thr Phe Trp Tyr His Ser
 115 120 125
 His Phe Gly Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Met Val Ile
 130 135 140
 Tyr Asp Asp Asn Asp Pro His Ala Ala Leu Tyr Asp Glu Asp Asp Glu
 145 150 155 160
 Asn Thr Ile Ile Thr Leu Ala Asp Trp Tyr His Ile Pro Ala Pro Ser

	165								170				175			
	Ile	Gln	Gly	Ala	Ala	Gln	Pro	Asp	Ala	Thr	Leu	Ile	Asn	Gly	Lys	Gly
				180					185					190		
5	Arg	Tyr	Val	Gly	Gly	Pro	Ala	Ala	Glu	Leu	Ser	Ile	Val	Asn	Val	Glu
			195					200					205			
	Gln	Gly	Lys	Lys	Tyr	Arg	Met	Arg	Leu	Ile	Ser	Leu	Ser	Cys	Asp	Pro
10		210					215					220				
	Asn	Trp	Gln	Phe	Ser	Ile	Asp	Gly	His	Glu	Leu	Thr	Ile	Ile	Glu	Val
	225					230					235				240	
15	Asp	Gly	Gln	Leu	Thr	Glu	Pro	His	Thr	Val	Asp	Arg	Leu	Gln	Ile	Phe
					245					250					255	
	Thr	Gly	Gln	Arg	Tyr	Ser	Phe	Val	Leu	Asp	Ala	Asn	Gln	Pro	Val	Asp
				260					265					270		
20	Asn	Tyr	Trp	Ile	Arg	Ala	Gln	Pro	Asn	Lys	Gly	Arg	Asn	Gly	Leu	Ala
			275					280					285			
	Gly	Thr	Phe	Ala	Asn	Gly	Val	Asn	Ser	Ala	Ile	Leu	Arg	Tyr	Ala	Gly
25		290					295					300				
	Ala	Ala	Asn	Ala	Asp	Pro	Thr	Thr	Ser	Ala	Asn	Pro	Asn	Pro	Ala	Gln
	305					310					315					320
30	Leu	Asn	Glu	Ala	Asp	Leu	His	Ala	Leu	Ile	Asp	Pro	Ala	Ala	Pro	Gly
					325					330					335	
	Ile	Pro	Thr	Pro	Gly	Ala	Ala	Asp	Val	Asn	Leu	Arg	Phe	Gln	Leu	Gly
				340					345					350		
35	Phe	Ser	Gly	Gly	Arg	Phe	Thr	Ile	Asn	Gly	Thr	Ala	Tyr	Glu	Ser	Pro
			355					360					365			
	Ser	Val	Pro	Thr	Leu	Leu	Gln	Ile	Met	Ser	Gly	Ala	Gln	Ser	Ala	Asn
40		370					375					380				
	Asp	Leu	Leu	Pro	Ala	Gly	Ser	Val	Tyr	Glu	Leu	Pro	Arg	Asn	Gln	Val
	385					390					395					400
45	Val	Glu	Leu	Val	Val	Pro	Ala	Gly	Val	Leu	Gly	Gly	Pro	His	Pro	Phe
					405					410					415	
	His	Leu	His	Gly	His	Ala	Phe	Ser	Val	Val	Arg	Ser	Ala	Gly	Ser	Ser
				420					425					430		
50	Thr	Tyr	Asn	Phe	Val	Asn	Pro	Val	Lys	Arg	Asp	Val	Val	Ser	Leu	Gly
			435					440					445			
	Val	Thr	Gly	Asp	Glu	Val	Thr	Ile	Arg	Phe	Val	Thr	Asp	Asn	Pro	Gly
55		450					455					460				
	Pro	Trp	Phe	Phe	His	Cys	His	Ile	Glu	Phe	His	Leu	Met	Asn	Gly	Leu
	465					470					475					480
60	Ala	Ile	Val	Phe	Ala	Glu	Asp	Met	Ala	Asn	Thr	Val	Asp	Ala	Asn	Asn
					485					490					495	
	Pro	Pro	Val	Glu	Trp	Ala	Gln	Leu	Cys	Glu	Ile	Tyr	Asp	Asp	Leu	Pro
				500					505					510		
65																
	Pro	Glu	Ala	Thr	Ser	Ile	Gln	Thr	Val	Val	Arg	Arg	Ala	Glu	Pro	Thr
			515					520					525			

Gly Phe Ser Ala Lys Phe Arg Arg Glu Gly Leu
 530 535

5 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
 (B) TYPE: amino acid
 10 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gly Ile Gly Pro Val Ala Asp Leu Thr Ile Thr Asn Ala Ala Val Ser
 1 5 10 15
 20 Pro Asp Gly Phe Ser Arg Gln Ala Val Val Val Asn Gly Gly Thr Pro
 20 25 30
 Gly Pro Leu Ile Thr Gly Asn Met Gly Asp Arg Phe Gln Leu Asn Val
 25 35 40 45
 Ile Asp Asn Leu Thr Asn His Thr Met Leu Lys Ser Thr Ser Ile His
 50 55 60
 30 Trp His Gly Phe Phe Gln Lys Gly Thr Asn Trp Ala Asp Gly Pro Ala
 65 70 75 80
 Phe Ile Asn Gln Cys Pro Ile Ser Ser Gly His Ser Phe Leu Tyr Asp
 85 90 95
 35 Phe Gln Val Pro Asp Gln Ala Gly Thr Phe Trp Tyr His Ser His Leu
 100 105 110
 Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Phe Val Val Tyr Asp
 115 120 125
 Pro Asn Asp Pro Ala Ala Asp Leu Tyr Asp Val Asp Asn Asp Asp Thr
 130 135 140
 45 Val Ile Thr Leu Val Asp Trp Tyr His Val Ala Ala Lys Leu Gly Pro
 145 150 155 160
 Ala Phe Pro Leu Gly Ala Asp Ala Thr Leu Ile Asn Gly Lys Gly Arg
 165 170 175
 50 Ser Pro Ser Thr Thr Thr Ala Asp Leu Ser Val Ile Ser Val Thr Pro
 180 185 190
 Gly Lys Arg Tyr Arg Phe Arg Leu Val Ser Leu Ser Cys Asp Pro Asn
 195 200 205
 Tyr Thr Phe Ser Ile Asp Gly His Asn Met Thr Ile Ile Glu Thr Asp
 210 215 220
 60 Ser Ile Asn Thr Ala Pro Leu Val Val Asp Ser Ile Gln Ile Phe Ala
 225 230 235 240
 Ala Gln Arg Tyr Ser Phe Val Leu Glu Ala Asn Gln Ala Val Asp Asn
 245 250 255
 65 Tyr Trp Ile Arg Ala Asn Pro Asn Phe Gly Asn Val Gly Phe Thr Gly
 260 265 270

143

Gly Ile Asn Ser Ala Ile Leu Arg Tyr Asp Gly Ala Ala Ala Val Glu
 275 280 285
 5 Pro Thr Thr Thr Gln Thr Thr Ser Thr Ala Pro Leu Asn Glu Val Asn
 290 295 300
 Leu His Pro Leu Val Thr Thr Ala Val Pro Gly Ser Pro Val Ala Gly
 305 310 315 320
 10 Gly Val Asp Leu Ala Ile Asn Met Ala Phe Asn Phe Asn Gly Thr Asn
 325 330 335
 Phe Phe Ile Asn Gly Ala Ser Phe Thr Pro Pro Thr Val Pro Val Leu
 340 345 350
 15 Leu Gln Ile Ile Ser Gly Ala Gln Asn Ala Gln Asp Leu Leu Pro Ser
 355 360 365
 Gly Ser Val Tyr Ser Leu Pro Ser Asn Ala Asp Ile Glu Ile Ser Phe
 370 375 380
 20 Pro Ala Thr Ala Ala Ala Pro Gly Ala Pro His Pro Phe His Leu His
 385 390 395 400
 25 Gly His Ala Phe Ala Val Val Arg Ser Ala Gly Ser Thr Val Tyr Asn
 405 410 415
 Tyr Asp Asn Pro Ile Phe Arg Asp Val Val Ser Thr Gly Thr Pro Ala
 420 425 430
 30 Ala Gly Asp Asn Val Thr Ile Arg Phe Arg Thr Asp Asn Pro Gly Pro
 435 440 445
 Trp Phe Leu His Cys His Ile Asp Phe His Leu Glu Ala Gly Phe Ala
 450 455 460
 35 Val Val Phe Ala Glu Asp Ile Pro Asp Val Ala Ser Ala Asn Pro Val
 465 470 475 480
 40 Pro Gln Ala Trp Ser Asp Leu Cys Pro Thr Tyr Asp Ala Leu Asp Pro
 485 490 495
 Ser Asp Gln

45

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 amino acids
 50 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

60 Ala Ile Gly Pro Val Ala Ser Leu Val Val Ala Asn Ala Pro Val Ser
 1 5 10 15
 Pro Asp Gly Phe Leu Arg Asp Ala Ile Val Val Asn Gly Val Val Pro
 20 25 30
 65 Ser Pro Leu Ile Thr Gly Lys Lys Gly Asp Arg Phe Gln Leu Asn Val
 35 40 45
 Val Asp Thr Leu Thr Asn His Ser Met Leu Lys Ser Thr Ser Ile His

	50		55		60											
	Trp 65	His	Gly	Phe	Phe	Gln 70	Ala	Gly	Thr	Asn	Trp 75	Ala	Glu	Gly	Pro	Ala 80
5	Phe	Val	Asn	Gln	Cys 85	Pro	Ile	Ala	Ser	Gly 90	His	Ser	Phe	Leu	Tyr	Asp 95
10	Phe	His	Val	Pro 100	Asp	Gln	Ala	Gly	Thr 105	Phe	Trp	Tyr	His	Ser 110	His	Leu
	Ser	Thr	Gln 115	Tyr	Cys	Asp	Gly	Leu	Arg	Gly 120	Pro	Phe	Val 125	Val	Tyr	Asp
15	Pro	Lys	Asp	Pro	His	Ala	Ser	Arg	Tyr	Asp	Val	Asp 140	Asn	Glu	Ser	Thr
20	Val	Ile	Thr	Leu	Thr	Asp 150	Trp	Tyr	His	Thr	Ala 155	Ala	Arg	Leu	Gly	Pro 160
	Lys	Phe	Pro	Leu	Gly 165	Ala	Asp	Ala	Thr	Leu 170	Ile	Asn	Gly	Leu	Gly 175	Arg
25	Ser	Ala	Ser	Thr 180	Pro	Thr	Ala	Ala	Leu	Ala 185	Val	Ile	Asn	Val 190	Gln	His
	Gly	Lys	Arg	Tyr 195	Arg	Phe	Arg	Leu	Val	Ser	Ile	Ser	Cys 205	Asp	Pro	Asn
30	Tyr	Thr	Phe	Ser	Ile	Asp	Gly 215	His	Asn	Leu	Thr	Val 220	Ile	Glu	Val	Asp
35	Gly	Ile	Asn	Ser	Gln 230	Pro	Leu	Leu	Val	Asp	Ser 235	Ile	Gln	Ile	Phe	Ala 240
	Ala	Gln	Arg	Tyr	Ser 245	Phe	Val	Leu	Asn	Ala 250	Asn	Gln	Thr	Val	Gly 255	Asn
40	Tyr	Trp	Val	Arg 260	Ala	Asn	Pro	Asn	Phe 265	Gly	Thr	Val	Gly	Phe 270	Ala	Gly
	Gly	Ile	Asn	Ser 275	Ala	Ile	Leu	Arg	Tyr 280	Gln	Gly	Ala	Pro 285	Val	Ala	Glu
45	Pro	Thr	Thr	Thr	Gln	Thr	Pro 295	Ser	Val	Ile	Pro	Leu 300	Ile	Glu	Thr	Asn
50	Leu	His	Pro	Leu	Ala	Arg	Met 310	Pro	Val	Pro	Gly 315	Ser	Pro	Thr	Pro	Gly 320
	Gly	Val	Asp	Lys	Ala 325	Leu	Asn	Leu	Ala	Phe 330	Asn	Phe	Asn	Gly	Thr 335	Asn
55	Phe	Phe	Ile	Asn	Asn	Ala	Thr	Phe	Thr 345	Pro	Pro	Thr	Val 350	Pro	Val	Leu
	Leu	Gln	Ile	Leu	Ser	Gly	Ala	Gln	Thr	Ala	Gln	Asp	Leu 365	Leu	Pro	Ala
60	Gly	Ser	Val	Tyr	Pro	Leu	Pro 375	Ala	His	Ser	Thr	Ile 380	Glu	Ile	Thr	Leu
65	Pro	Ala	Thr	Ala	Leu	Ala	Pro 390	Gly	Ala	Pro	His 395	Pro	Phe	His	Leu	His 400
	Gly	His	Ala	Phe	Ala	Val	Val	Arg	Ser	Ala	Gly	Ser	Thr	Thr	Tyr	Asn 415
					405					410						

Tyr Asn Asp Pro Ile Phe Arg Asp Val Val Ser Thr Gly Thr Pro Ala
 420 425 430
 5 Ala Gly Asp Asn Val Thr Ile Arg Phe Gln Thr Asp Asn Pro Gly Pro
 435 440 445
 Trp Phe Leu His Cys His Ile Asp Phe His Leu Asp Ala Gly Phe Ala
 450 455 460
 10 Ile Val Phe Ala Glu Asp Val Ala Asp Val Lys Ala Ala Asn Pro Val
 465 470 475 480
 15 Pro Lys Ala Trp Ser Asp Leu Cys Pro Ile Tyr Asp Gly Leu Ser Glu
 485 490 495
 Ala Asn Gln

20 (2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 548 amino acids
 (B) TYPE: amino acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met His Thr Phe Leu Arg Ser Thr Ala Leu Val Val Ala Gly Leu Ser
 1 5 10 15
 35 Ala Arg Ala Leu Ala Ser Ile Gly Pro Val Thr Asp Phe His Ile Val
 20 25 30
 40 Asn Ala Ala Val Ser Pro Asp Gly Phe Ser Arg Gln Ala Val Leu Ala
 35 40 45
 Glu Gly Val Phe Pro Gly Pro Leu Ile Ala Gly Asn Lys Gly Asp Asn
 50 55 60
 45 Phe Gln Ile Asn Val Ile Asp Glu Leu Thr Asn Ala Thr Met Leu Lys
 65 70 75 80
 Thr Thr Thr Ile His Trp His Gly Phe Phe Gln His Gly Thr Asn Trp
 85 90 95
 50 Ala Asp Gly Pro Ala Phe Ile Asn Gln Cys Pro Ile Ala Ser Gly Asp
 100 105 110
 55 Ser Phe Leu Tyr Asn Phe Gln Val Pro Asp Gln Ala Gly Thr Phe Trp
 115 120 125
 Tyr His Ser His Leu Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro
 130 135 140
 60 Phe Val Val Tyr Asp Pro Ala Asp Pro Tyr Leu Asp Gln Tyr Asp Val
 145 150 155 160
 Asp Asp Asp Ser Thr Val Ile Thr Leu Ala Asp Trp Tyr His Thr Ala
 165 170 175
 65 Ala Arg Leu Gly Ser Pro Phe Pro Ala Ala Asp Thr Thr Leu Ile Asn
 180 185 190

Gly Leu Gly Arg Cys Gly Glu Ala Gly Cys Pro Val Ser Asp Leu Ala
 195 200 205
 5 Val Ile Ser Val Thr Lys Gly Lys Arg Tyr Arg Phe Arg Leu Val Ser
 210 215 220
 Ile Ser Cys Asp Ser Phe Phe Thr Phe Ser Ile Asp Gly His Ser Leu
 225 230 235 240
 10 Asn Val Ile Glu Val Asp Ala Thr Asn His Gln Pro Leu Thr Val Asp
 245 250 255
 Glu Leu Thr Ile Tyr Ala Gly Gln Arg Tyr Ser Phe Ile Leu Thr Ala
 260 265 270
 15 Asp Gln Asp Val Asp Asn Tyr Trp Ile Arg Ala Asn Pro Gly Ile Gly
 275 280 285
 Ile Thr Thr Gly Phe Ala Gly Gly Ile Asn Ser Ala Ile Leu Arg Tyr
 290 295 300
 Asp Gly Ala Asp Val Val Glu Pro Thr Thr Thr Gln Ala Thr Ser Pro
 305 310 315 320
 25 Val Val Leu Ser Glu Ser Asn Leu Ala Pro Leu Thr Asn Ala Ala Ala
 325 330 335
 Pro Gly Leu Pro Glu Val Gly Gly Val Asp Leu Ala Leu Asn Phe Asn
 340 345 350
 30 Leu Thr Phe Asp Gly Pro Ser Leu Lys Phe Gln Ile Asn Gly Val Thr
 355 360 365
 Phe Val Pro Pro Thr Val Pro Val Leu Leu Gln Ile Leu Ser Gly Ala
 370 375 380
 35 Gln Ser Ala Ala Asp Leu Leu Pro Ser Gly Ser Val Tyr Ala Leu Pro
 385 390 395 400
 40 Ser Asn Ala Thr Ile Glu Leu Ser Leu Pro Ala Gly Ala Leu Gly Gly
 405 410 415
 Pro His Pro Phe His Leu His Gly His Thr Phe Ser Val Val Arg Pro
 420 425 430
 45 Ala Gly Ser Thr Thr Tyr Asn Tyr Val Asn Pro Val Gln Arg Asp Val
 435 440 445
 Val Ser Ile Gly Asn Thr Gly Asp Asn Val Thr Ile Arg Phe Asp Thr
 450 455 460
 Asn Asn Pro Gly Pro Trp Phe Leu His Cys His Ile Asp Trp His Leu
 465 470 475 480
 55 Glu Ala Ala Leu Pro Leu Ser Ser Leu Arg Thr Ser Leu Thr Leu Arg
 485 490 495
 Pro Leu Thr Leu Ser Pro Arg Thr Gly Pro Thr Cys Ala Leu Ser Thr
 500 505 510
 60 Thr Leu Trp Thr His Leu Ile Thr Ser Gly Phe Ala Ser Ile Ile Gln
 515 520 525
 65 Trp Met Met Gly Gly Asn Gly Leu Phe Ala Pro His Ala Leu Ser Phe
 530 535 540
 Leu Gly Ser Gln

545

(2) INFORMATION FOR SEQ ID NO: 5:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Leu Ser Ser Ile Thr Leu Leu Pro Leu Leu Ala Ala Val Ser Thr
 1 5 10 15

Pro Ala Phe Ala Ala Val Arg Asn Tyr Lys Phe Asp Ile Lys Asn Val
 20 20 25 30

Asn Val Ala Pro Asp Gly Phe Gln Arg Ser Ile Val Ser Val Asn Gly
 35 40 45

Leu Val Pro Gly Thr Leu Ile Thr Ala Asn Lys Gly Asp Thr Leu Arg
 50 55 60

Ile Asn Val Thr Asn Gln Leu Thr Asp Pro Ser Met Arg Arg Ala Thr
 65 70 75 80

Thr Ile His Trp His Gly Leu Phe Gln Ala Thr Thr Ala Asp Glu Asp
 85 90 95

Gly Pro Ala Phe Val Thr Gln Cys Pro Ile Ala Gln Asn Leu Ser Tyr
 100 105 110

Thr Tyr Glu Ile Pro Leu Arg Gly Gln Thr Gly Thr Met Trp Tyr His
 115 120 125

Ala His Leu Ala Ser Gln Tyr Val Asp Gly Leu Arg Gly Pro Leu Val
 130 135 140

Ile Tyr Asp Pro Asn Asp Pro His Lys Ser Arg Tyr Asp Val Asp Asp
 145 150 155 160

Ala Ser Thr Val Val Met Leu Glu Asp Trp Tyr His Thr Pro Ala Pro
 165 170 175

Val Leu Glu Lys Gln Met Phe Ser Thr Asn Asn Thr Ala Leu Leu Ser
 180 185 190

Pro Val Pro Asp Ser Gly Leu Ile Asn Gly Lys Gly Arg Tyr Val Gly
 195 200 205

Gly Pro Ala Val Pro Arg Ser Val Ile Asn Val Lys Arg Gly Lys Arg
 210 215 220

Tyr Arg Leu Arg Val Ile Asn Ala Ser Ala Ile Gly Ser Phe Thr Phe
 225 230 235 240

Ser Ile Glu Gly His Ser Leu Thr Val Ile Glu Ala Asp Gly Ile Leu
 245 250 255

His Gln Pro Leu Ala Val Asp Ser Phe Gln Ile Tyr Ala Gly Gln Arg
 260 265 270

Tyr Ser Val Ile Val Glu Ala Asn Gln Thr Ala Ala Asn Tyr Trp Ile
 275 280 285

Arg Ala Pro Met Thr Val Ala Gly Ala Gly Thr Asn Ala Asn Leu Asp
 290 295 300
 5 Pro Thr Asn Val Phe Ala Val Leu His Tyr Glu Gly Ala Pro Asn Ala
 305 310 315 320
 Glu Pro Thr Thr Glu Gln Gly Ser Ala Ile Gly Thr Ala Leu Val Glu
 325 330 335
 10 Glu Asn Leu His Ala Leu Ile Asn Pro Gly Ala Pro Gly Gly Ser Ala
 340 345 350
 Pro Ala Asp Val Ser Leu Asn Leu Ala Ile Gly Arg Ser Thr Val Asp
 355 360 365
 15 Gly Ile Leu Arg Phe Thr Phe Asn Asn Ile Lys Tyr Glu Ala Pro Ser
 370 375 380
 20 Leu Pro Thr Leu Leu Lys Ile Leu Ala Asn Asn Ala Ser Asn Asp Ala
 385 390 395 400
 Asp Phe Thr Pro Asn Glu His Thr Ile Val Leu Pro His Asn Lys Val
 405 410 415
 25 Ile Glu Leu Asn Ile Thr Gly Gly Ala Asp His Pro Ile His Leu His
 420 425 430
 Gly His Val Phe Asp Ile Val Lys Ser Leu Gly Gly Thr Pro Asn Tyr
 435 440 445
 30 Val Asn Pro Pro Arg Arg Asp Val Val Arg Val Gly Gly Thr Gly Val
 450 455 460
 35 Val Leu Arg Phe Lys Thr Asp Asn Pro Gly Pro Trp Phe Val His Cys
 465 470 475 480
 His Ile Asp Trp His Leu Glu Ala Gly Leu Ala Leu Val Phe Ala Glu
 485 490 495
 40 Ala Pro Ser Gln Ile Arg Gln Gly Val Gln Ser Val Gln Pro Asn Asn
 500 505 510
 Ala Trp Asn Gln Leu Cys Pro Lys Tyr Ala Ala Leu Pro Pro Asp Leu
 515 520 525
 45 Gln

50 (2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 599 amino acids
 (B) TYPE: amino acid
 55 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Arg Ser Thr Thr Ser Leu Phe Ala Leu Ser Leu Val Ala Ser
 1 5 10 15
 65 Ala Phe Ala Arg Val Val Asp Tyr Gly Phe Asp Val Ala Asn Gly Ala
 20 25 30
 Val Ala Pro Asp Gly Val Thr Arg Asn Ala Val Leu Val Asn Gly Arg

	35							40					45				
5	Phe	Pro	Gly	Pro	Leu	Ile	Thr	Ala	Asn	Lys	Gly	Asp	Thr	Leu	Lys	Ile	
	50						55					60					
	Thr	Val	Arg	Asn	Lys	Leu	Ser	Asp	Pro	Thr	Met	Arg	Arg	Ser	Thr	Thr	
	65					70					75					80	
10	Ile	His	Trp	His	Gly	Leu	Leu	Gln	His	Arg	Thr	Ala	Glu	Glu	Asp	Gly	
					85					90					95		
	Pro	Ala	Phe	Val	Thr	Gln	Cys	Pro	Ile	Pro	Pro	Gln	Glu	Ser	Tyr	Thr	
				100					105					110			
15	Tyr	Thr	Met	Pro	Leu	Gly	Glu	Gln	Thr	Gly	Thr	Tyr	Trp	Tyr	His	Ser	
			115					120					125				
	His	Leu	Ser	Ser	Gln	Tyr	Val	Asp	Gly	Leu	Arg	Gly	Pro	Ile	Val	Ile	
		130					135					140					
20	Tyr	Asp	Pro	His	Asp	Pro	Tyr	Arg	Asn	Tyr	Tyr	Asp	Val	Asp	Asp	Glu	
	145					150					155					160	
	Arg	Thr	Val	Phe	Thr	Leu	Ala	Asp	Trp	Tyr	His	Thr	Pro	Ser	Glu	Ala	
25					165					170					175		
	Ile	Ile	Ala	Thr	His	Asp	Val	Leu	Lys	Thr	Ile	Pro	Asp	Ser	Gly	Thr	
				180					185					190			
30	Ile	Asn	Gly	Lys	Gly	Lys	Tyr	Asp	Pro	Ala	Ser	Ala	Asn	Thr	Asn	Asn	
			195					200					205				
	Thr	Thr	Leu	Glu	Asn	Leu	Tyr	Thr	Leu	Lys	Val	Lys	Arg	Gly	Lys	Arg	
		210					215					220					
35	Tyr	Arg	Leu	Arg	Ile	Ile	Asn	Ala	Ser	Ala	Ile	Ala	Ser	Phe	Arg	Phe	
	225					230					235					240	
	Gly	Val	Gln	Gly	His	Lys	Cys	Thr	Ile	Ile	Glu	Ala	Asp	Gly	Val	Leu	
40					245					250					255		
	Thr	Lys	Pro	Ile	Glu	Val	Asp	Ala	Phe	Asp	Ile	Leu	Ala	Gly	Gln	Arg	
				260					265					270			
45	Tyr	Ser	Cys	Ile	Leu	Lys	Ala	Asp	Gln	Asp	Pro	Asp	Ser	Tyr	Trp	Ile	
			275					280					285				
	Asn	Ala	Pro	Ile	Thr	Asn	Val	Leu	Asn	Thr	Asn	Val	Gln	Ala	Leu	Leu	
		290					295					300					
50	Val	Tyr	Glu	Asp	Asp	Lys	Arg	Pro	Thr	His	Tyr	Pro	Trp	Lys	Pro	Phe	
	305					310					315					320	
	Leu	Thr	Trp	Lys	Ile	Ser	Asn	Glu	Ile	Ile	Gln	Tyr	Trp	Gln	His	Lys	
55					325					330					335		
	His	Gly	Ser	His	Gly	His	Lys	Gly	Lys	Gly	His	His	His	Lys	Val	Arg	
				340					345					350			
60	Ala	Ile	Gly	Gly	Val	Ser	Gly	Leu	Ser	Ser	Arg	Val	Lys	Ser	Arg	Ala	
			355					360					365				
	Ser	Asp	Leu	Ser	Lys	Lys	Ala	Val	Glu	Leu	Ala	Ala	Ala	Leu	Val	Ala	
		370					375					380					
65	Gly	Glu	Ala	Glu	Leu	Asp	Lys	Arg	Gln	Asn	Glu	Asp	Asn	Ser	Thr	Ile	
	385					390					395					400	
	Val	Leu	Asp	Glu	Thr	Lys	Leu	Ile	Pro	Leu	Val	Gln	Pro	Gly	Ala	Pro	

	405	410	415
	Gly Gly Ser Arg Pro Ala Asp Val Val Val Pro Leu Asp Phe Gly Leu		
5	420	425	430
	Asn Phe Ala Asn Gly Leu Trp Thr Ile Asn Asn Val Ser Tyr Ser Pro		
	435	440	445
10	Pro Asp Val Pro Thr Leu Leu Lys Ile Leu Thr Asp Lys Asp Lys Val		
	450	455	460
	Asp Ala Ser Asp Phe Thr Ala Asp Glu His Thr Tyr Ile Leu Pro Lys		
	465	470	475
15	Asn Gln Val Val Glu Leu His Ile Lys Gly Gln Ala Leu Gly Ile Val		
	485	490	495
	His Pro Leu His Leu His Gly His Ala Phe Asp Val Val Gln Phe Gly		
20	500	505	510
	Asp Asn Ala Pro Asn Tyr Val Asn Pro Pro Arg Arg Asp Val Val Gly		
	515	520	525
25	Val Thr Asp Ala Gly Val Arg Ile Gln Phe Arg Thr Asp Asn Pro Gly		
	530	535	540
	Pro Trp Phe Leu His Cys His Ile Asp Trp His Leu Glu Glu Gly Phe		
	545	550	555
30	Ala Met Val Phe Ala Glu Ala Pro Glu Asp Ile Lys Lys Gly Ser Gln		
	565	570	575
	Ser Val Lys Pro Asp Gly Gln Trp Lys Lys Leu Cys Glu Lys Tyr Glu		
35	580	585	590
	Lys Leu Pro Glu Ala Leu Gln		
	595		

(2) INFORMATION FOR SEQ ID NO: 7:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 amino acids

(B) TYPE: amino acid

45 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met	Ala	Arg	Thr	Thr	Phe	Leu	Val	Ser	Val	Ser	Leu	Phe	Val	Ser	Ala
1				5					10					15	
Val	Leu	Ala	Arg	Thr	Val	Glu	Tyr	Asn	Leu	Lys	Ile	Ser	Asn	Gly	Lys
20								25					30		
Ile	Ala	Pro	Asp	Gly	Val	Glu	Arg	Asp	Ala	Thr	Leu	Val	Asn	Gly	Gly
35							40					45			
Tyr	Pro	Gly	Pro	Leu	Ile	Phe	Ala	Asn	Lys	Gly	Asp	Thr	Leu	Lys	Val
50						55					60				
Lys	Val	Gln	Asn	Lys	Leu	Thr	Asn	Pro	Asp	Met	Tyr	Arg	Thr	Thr	Ser
65					70					75					80
Ile	His	Trp	His	Gly	Leu	Leu	Gln	His	Arg	Asn	Ala	Asp	Asp	Asp	Gly
				85					90					95	

	Pro	Ala	Phe	Val	Thr	Gln	Cys	Pro	Ile	Val	Pro	Gln	Ala	Ser	Tyr	Thr	
				100					105					110			
5	Tyr	Thr	Met	Pro	Leu	Gly	Asp	Gln	Thr	Gly	Thr	Tyr	Trp	Tyr	His	Ser	
			115					120					125				
	His	Leu	Ser	Ser	Gln	Tyr	Val	Asp	Gly	Leu	Arg	Gly	Pro	Leu	Val	Ile	
		130					135					140					
10	Tyr	Asp	Pro	Lys	Asp	Pro	His	Arg	Arg	Leu	Tyr	Asp	Ile	Asp	Asp	Glu	
		145				150					155					160	
	Lys	Thr	Val	Leu	Ile	Ile	Gly	Asp	Trp	Tyr	His	Thr	Ser	Ser	Lys	Ala	
15					165					170					175		
	Ile	Leu	Ala	Thr	Gly	Asn	Ile	Thr	Leu	Gln	Gln	Pro	Asp	Ser	Ala	Thr	
				180					185					190			
20	Ile	Asn	Gly	Lys	Gly	Arg	Phe	Asp	Pro	Asp	Asn	Thr	Pro	Ala	Asn	Pro	
			195					200					205				
	Asn	Thr	Leu	Tyr	Thr	Leu	Lys	Val	Lys	Arg	Gly	Lys	Arg	Tyr	Arg	Leu	
		210					215					220					
25	Arg	Val	Ile	Asn	Ser	Ser	Ala	Ile	Ala	Ser	Phe	Arg	Met	Ser	Ile	Gln	
		225				230					235					240	
	Gly	His	Lys	Met	Thr	Val	Ile	Ala	Ala	Asp	Gly	Val	Ser	Thr	Lys	Pro	
30					245					250					255		
	Tyr	Gln	Val	Asp	Ser	Phe	Asp	Ile	Leu	Ala	Gly	Gln	Arg	Ile	Asp	Ala	
				260					265					270			
35	Val	Val	Glu	Ala	Asn	Gln	Glu	Pro	Asp	Thr	Tyr	Trp	Ile	Asn	Ala	Pro	
			275					280					285				
	Leu	Thr	Asn	Val	Ala	Asn	Lys	Thr	Ala	Gln	Ala	Leu	Leu	Ile	Tyr	Glu	
		290					295					300					
40	Asp	Asp	Arg	Arg	Pro	Tyr	His	Pro	Pro	Lys	Gly	Pro	Tyr	Arg	Lys	Trp	
		305				310					315					320	
	Ser	Val	Ser	Glu	Ala	Ile	Ile	Lys	Tyr	Trp	Lys	His	Lys	His	Gly	Arg	
45					325					330					335		
	Gly	Leu	Leu	Ser	Gly	His	Gly	Gly	Leu	Lys	Ala	Arg	Met	Met	Glu	Gly	
				340					345					350			
50	Ser	Leu	His	Leu	His	Gly	Arg	Arg	Asp	Ile	Val	Lys	Arg	Gln	Asn	Glu	
			355					360					365				
	Thr	Thr	Thr	Val	Val	Met	Asp	Glu	Thr	Lys	Leu	Val	Pro	Leu	Glu	His	
		370					375					380					
55																	
	Pro	Gly	Ala	Ala	Cys	Gly	Ser	Lys	Pro	Ala	Asp	Leu	Val	Ile	Asp	Leu	
		385				390					395					400	
60	Thr	Phe	Gly	Val	Asn	Phe	Thr	Thr	Gly	His	Trp	Met	Ile	Asn	Gly	Ile	
					405					410					415		
	Pro	His	Lys	Ser	Pro	Asp	Met	Pro	Thr	Leu	Leu	Lys	Ile	Leu	Thr	Asp	
				420					425					430			
65	Thr	Asp	Gly	Val	Thr	Glu	Ser	Asp	Phe	Thr	Gln	Pro	Glu	His	Thr	Ile	
			435					440					445				

Ile Leu Pro Lys Asn Lys Cys Val Glu Phe Asn Ile Lys Gly Asn Ser
 450 455 460

5 Gly Leu Gly Ile Val His Pro Ile His Leu His Gly His Thr Phe Asp
 465 470 475 480

Val Val Gln Phe Gly Asn Asn Pro Pro Asn Tyr Val Asn Pro Pro Arg
 485 490 495

10 Arg Asp Val Val Gly Ala Thr Asp Glu Gly Val Arg Phe Gln Phe Lys
 500 505 510

Thr Asp Asn Pro Gly Pro Trp Phe Leu His Cys His Ile Asp Trp His
 515 520 525

15 Leu Glu Glu Gly Phe Ala Met Val Phe Ala Glu Ala Pro Glu Ala Ile
 530 535 540

20 Lys Gly Gly Pro Lys Ser Val Pro Val Asp Arg Gln Trp Lys Asp Leu
 545 550 555 560

Cys Arg Lys Tyr Gly Ser Leu Pro Ala Gly Phe Leu
 565 570

25 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 575 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Arg Thr Thr Phe Leu Val Ser Val Ser Leu Phe Val Ser Ala
 1 5 10 15

Val Leu Ala Arg Thr Val Glu Tyr Gly Leu Lys Ile Ser Asp Gly Glu
 20 25 30

Ile Ala Pro Asp Gly Val Lys Arg Asn Ala Thr Leu Val Asn Gly Gly
 35 40 45

Tyr Pro Gly Pro Leu Ile Phe Ala Asn Lys Gly Asp Thr Leu Lys Val
 50 55 60

Lys Val Gln Asn Lys Leu Thr Asn Pro Glu Met Tyr Arg Thr Thr Ser
 65 70 75 80

Ile His Trp His Gly Leu Leu Gln His Arg Asn Ala Asp Asp Asp Gly
 85 90 95

Pro Ser Phe Val Thr Gln Cys Pro Ile Val Pro Arg Glu Ser Tyr Thr
 100 105 110

Tyr Thr Ile Pro Leu Asp Asp Gln Thr Gly Thr Tyr Trp Tyr His Ser
 115 120 125

His Leu Ser Ser Gln Tyr Val Asp Gly Leu Arg Gly Pro Leu Val Ile
 130 135 140

65 Tyr Pro Lys Asp Pro His Arg Arg Leu Tyr Asp Val Asp Asp Glu Lys
 145 150 155 160

Thr Val Leu Ile Ile Gly Asp Trp Tyr His Glu Ser Ser Lys Ala Ile

					165					170						175				
					Leu	Ala	Ser	Gly	Asn	Ile	Thr	Arg	Gln	Arg	Pro	Val	Ser	Ala	Thr	Ile
					180								185					190		
5					Asn	Gly	Lys	Gly	Arg	Phe	Asp	Pro	Asp	Asn	Thr	Pro	Ala	Asn	Pro	Asp
					195							200					205			
					Thr	Leu	Tyr	Thr	Leu	Lys	Val	Lys	Arg	Gly	Lys	Arg	Tyr	Arg	Leu	Arg
10					210						215					220				
					Val	Ile	Asn	Ser	Ser	Glu	Ile	Ala	Ser	Phe	Arg	Phe	Ser	Val	Glu	Gly
					225					230					235					240
					His	Lys	Val	Thr	Val	Ile	Ala	Ala	Asp	Gly	Val	Ser	Thr	Lys	Pro	Tyr
15									245					250					255	
					Gln	Val	Asp	Ala	Phe	Asp	Ile	Leu	Ala	Gly	Gln	Arg	Ile	Asp	Cys	Val
									260				265					270		
20					Val	Glu	Ala	Asn	Gln	Glu	Pro	Asp	Thr	Tyr	Trp	Ile	Asn	Ala	Pro	Leu
							275					280					285			
					Thr	Asn	Val	Pro	Asn	Lys	Thr	Ala	Gln	Ala	Leu	Leu	Val	Tyr	Glu	Glu
25						290					295					300				
					Asp	Arg	Arg	Pro	Tyr	His	Pro	Pro	Lys	Gly	Pro	Tyr	Arg	Lys	Trp	Ser
					305					310					315					320
30					Val	Ser	Glu	Ala	Ile	Ile	Lys	Tyr	Trp	Asn	His	Lys	His	Lys	His	Gly
									325					330					335	
					Arg	Gly	Leu	Leu	Ser	Gly	His	Gly	Gly	Leu	Lys	Ala	Arg	Met	Ile	Glu
									340				345					350		
35					Gly	Ser	His	His	Leu	His	Ser	Arg	Ser	Val	Val	Lys	Arg	Gln	Asn	Glu
							355					360					365			
					Thr	Thr	Thr	Val	Val	Met	Asp	Glu	Ser	Lys	Leu	Val	Pro	Leu	Glu	Tyr
40						370					375					380				
					Pro	Gly	Ala	Ala	Cys	Gly	Ser	Lys	Pro	Ala	Asp	Leu	Val	Leu	Asp	Leu
										390					395					400
45					Thr	Phe	Gly	Leu	Asn	Phe	Ala	Thr	Gly	His	Trp	Met	Ile	Asn	Gly	Ile
									405					410					415	
					Pro	Tyr	Glu	Ser	Pro	Lys	Ile	Pro	Thr	Leu	Leu	Lys	Ile	Leu	Thr	Asp
								420					425					430		
50					Glu	Asp	Gly	Val	Thr	Glu	Ser	Asp	Phe	Thr	Lys	Glu	Glu	His	Thr	Val
							435					440					445			
					Ile	Leu	Pro	Lys	Asn	Lys	Cys	Ile	Glu	Phe	Asn	Ile	Lys	Gly	Asn	Ser
55						450					455					460				
					Gly	Ile	Pro	Ile	Thr	His	Pro	Val	His	Leu	His	Gly	His	Thr	Trp	Asp
									470					475						480
60					Val	Val	Gln	Phe	Gly	Asn	Asn	Pro	Pro	Asn	Tyr	Val	Asn	Pro	Pro	Arg
									485					490					495	
					Arg	Asp	Val	Val	Gly	Ser	Thr	Asp	Ala	Gly	Val	Arg	Ile	Gln	Phe	Lys
65									500				505					510		
					Thr	Asp	Asn	Pro	Gly	Pro	Trp	Phe	Leu	His	Cys	His	Ile	Asp	Trp	His
							515					520					525			

Leu Glu Glu Gly Phe Ala Met Val Phe Ala Glu Ala Pro Glu Ala Val
 530 535 540

5 Lys Gly Gly Pro Lys Ser Val Ala Val Asp Ser Gln Trp Glu Gly Leu
 545 550 555 560

Cys Gly Lys Tyr Asp Asn Trp Leu Lys Ser Asn Pro Gly Gln Leu
 565 570 575

10 (2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 616 amino acids
 15 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

25 Met Lys Arg Phe Phe Ile Asn Ser Leu Leu Leu Leu Ala Gly Leu Leu
 1 5 10 15

Asn Ser Gly Ala Leu Ala Ala Pro Ser Thr His Pro Arg Ser Asn Pro
 20 25 30

30 Asp Ile Leu Leu Glu Arg Asp Asp His Ser Leu Thr Ser Arg Gln Gly
 35 40

Ser Cys His Ser Pro Ser Asn Arg Ala Cys Trp Cys Ser Gly Phe Asp
 50 55 60

35 Ile Asn Thr Asp Tyr Glu Thr Lys Thr Pro Asn Thr Gly Val Val Arg
 65 70 75 80

40 Arg Tyr Thr Phe Asp Ile Thr Glu Val Asp Asn Arg Pro Gly Pro Asp
 85 90 95

Gly Val Ile Lys Glu Lys Leu Met Leu Ile Asn Asp Lys Leu Leu Gly
 100 105 110

45 Pro Thr Val Phe Ala Asn Trp Gly Asp Thr Ile Glu Val Thr Val Asn
 115 120 125

Asn His Leu Arg Thr Asn Gly Thr Ser Ile His Trp His Gly Leu His
 130 135 140

50 Gln Lys Gly Thr Asn Tyr His Asp Gly Ala Asn Gly Val Thr Glu Cys
 145 150 155 160

55 Pro Ile Pro Pro Gly Gly Ser Arg Val Tyr Ser Phe Arg Ala Arg Gln
 165 170 175

Tyr Gly Thr Ser Trp Tyr His Ser His Phe Ser Ala Gln Tyr Gly Asn
 180 185 190

60 Gly Val Ser Gly Ala Ile Gln Ile Asn Gly Pro Ala Ser Leu Pro Tyr
 195 200 205

Asp Ile Asp Leu Gly Val Leu Pro Leu Xaa Asp Trp Tyr Tyr Lys Ser
 210 215 220

65 Ala Asp Gln Leu Val Ile Glu Thr Leu Xaa Lys Gly Asn Ala Pro Phe
 225 230 235 240

	Ser	Asp	Asn	Val	Leu	Ile	Asn	Gly	Thr	Ala	Lys	His	Pro	Thr	Thr	Gly	
					245					250					255		
5	Glu	Gly	Glu	Tyr	Ala	Ile	Val	Lys	Leu	Thr	Pro	Asp	Lys	Arg	His	Arg	
				260					265					270			
	Leu	Arg	Leu	Ile	Asn	Met	Ser	Val	Glu	Asn	His	Phe	Gln	Val	Ser	Leu	
			275					280					285				
10	Ala	Lys	His	Thr	Met	Thr	Val	Ile	Ala	Ala	Asp	Met	Val	Pro	Val	Asn	
		290					295					300					
	Ala	Met	Thr	Val	Asp	Ser	Leu	Phe	Met	Ala	Val	Gly	Gln	Arg	Tyr	Asp	
	305					310				315						320	
15	Val	Thr	Ile	Asp	Ala	Ser	Gln	Ala	Val	Gly	Asn	Tyr	Trp	Phe	Asn	Ile	
					325					330					335		
20	Thr	Phe	Gly	Gly	Gln	Gln	Lys	Cys	Gly	Phe	Ser	His	Asn	Pro	Ala	Pro	
				340					345					350			
	Ala	Ala	Ile	Phe	Arg	Tyr	Glu	Gly	Ala	Pro	Asp	Ala	Leu	Pro	Thr	Asp	
			355					360					365				
25	Pro	Gly	Ala	Ala	Pro	Lys	Asp	His	Gln	Cys	Leu	Asp	Thr	Leu	Asp	Leu	
		370					375					380					
	Ser	Pro	Val	Val	Gln	Lys	Asn	Val	Pro	Val	Asp	Gly	Phe	Val	Lys	Glu	
	385					390					395					400	
30	Pro	Gly	Asn	Thr	Leu	Pro	Val	Thr	Leu	His	Val	Asp	Gln	Ala	Ala	Ala	
					405				410						415		
	Pro	His	Val	Phe	Thr	Trp	Lys	Ile	Asn	Gly	Ser	Ala	Ala	Asp	Val	Asp	
35				420					425					430			
	Trp	Asp	Arg	Pro	Val	Leu	Glu	Tyr	Val	Met	Asn	Asn	Asp	Leu	Ser	Ser	
			435					440					445				
40	Ile	Pro	Val	Lys	Asn	Asn	Ile	Val	Arg	Val	Asp	Gly	Val	Asn	Glu	Trp	
		450					455					460					
	Thr	Tyr	Trp	Leu	Val	Glu	Asn	Asp	Pro	Glu	Gly	Arg	Leu	Ser	Leu	Pro	
	465					470					475					480	
45	His	Pro	Met	His	Leu	His	Gly	His	Asp	Phe	Phe	Val	Leu	Gly	Arg	Ser	
					485					490					495		
	Pro	Asp	Val	Ser	Pro	Asp	Ser	Glu	Thr	Arg	Phe	Val	Phe	Asp	Pro	Ala	
50				500					505					510			
	Val	Asp	Leu	Pro	Arg	Leu	Arg	Gly	His	Asn	Pro	Val	Arg	Arg	Asp	Val	
			515					520					525				
55	Thr	Met	Leu	Pro	Ala	Arg	Gly	Trp	Leu	Leu	Leu	Ala	Phe	Arg	Thr	Asp	
		530					535					540					
	Asn	Pro	Gly	Ala	Trp	Leu	Phe	His	Cys	His	Ile	Ala	Xaa	His	Val	Ser	
60		545				550					555					560	
	Gly	Gly	Leu	Ser	Val	Asp	Phe	Leu	Glu	Arg	Pro	Asp	Glu	Leu	Arg	Gly	
					565					570					575		
65	Gln	Leu	Thr	Gly	Glu	Ser	Lys	Ala	Glu	Leu	Glu	Arg	Val	Cys	Arg	Glu	
				580					585					590			
	Trp	Lys	Asp	Trp	Glu	Ala	Lys	Ser	Pro	His	Gly	Lys	Ile	Asp	Ser	Gly	

595

600

605

Leu Lys Gln Arg Arg Trp Asp Ala
610 615

5

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

20 Gln Gln Ser Cys Asn Thr Pro Ser Asn Arg Ala Cys Trp Thr Asp Gly
1 5 10 15
 Tyr Asp Ile Asn Thr Asp Tyr Glu Val Asp Ser Pro Asp Thr Gly Val
20 25 30
 25 Val Arg Pro Tyr Thr Leu Thr Leu Thr Glu Val Asp Asn Trp Thr Gly
35 40 45
 Pro Asp Gly Val Val Lys Glu Lys Val Met Leu Val Asn Asn Ser Ile
50 55 60
 30 Ile Gly Pro Thr Ile Phe Ala Asp Trp Gly Asp Thr Ile Gln Val Thr
65 70 75 80
 Val Ile Asn Asn Leu Glu Thr Asn Gly Thr Ser Ile His Trp His Gly
35 85 90 95
 Leu His Gln Lys Gly Thr Asn Leu His Asp Gly Ala Asn Gly Ile Thr
100 105 110
 40 Glu Cys Pro Ile Pro Pro Lys Gly Gly Arg Lys Val Tyr Arg Phe Lys
115 120 125
 Ala Gln Gln Tyr Gly Thr Ser Trp Tyr His Ser His Phe Ser Ala Gln
130 135 140
 45 Tyr Gly Asn Gly Val Val Gly Ala Ile Gln Ile Asn Gly Pro Ala Ser
145 150 155 160
 Leu Pro Tyr Asp Thr Asp Leu Gly Val Phe Pro Ile Ser Asp Tyr Tyr
50 165 170 175
 Tyr Ser Ser Ala Asp Glu Leu Val Glu Leu Thr Lys Asn Ser Gly Ala
180 185 190
 55 Pro Phe Ser Asp Asn Val Leu Phe Asn Gly Thr Ala Lys His Pro Glu
195 200 205
 Thr Gly Glu Gly Glu Tyr Ala Asn Val Thr Leu Thr Pro Gly Arg Arg
210 215 220
 60 His Arg Leu Arg Leu Ile Asn Thr Ser Val Glu Asn His Phe Gln Val
225 230 235 240
 Ser Leu Val Asn His Thr Met Cys Ile Ile Ala Ala Asp Met Val Pro
65 245 250 255
 Val Asn Ala Met Thr Val Asp Ser Leu Phe Leu Gly Val Gly Gln Arg
260 265 270

	Tyr	Asp	Val	Val	Ile	Glu	Ala	Asn	Arg	Thr	Pro	Gly	Asn	Tyr	Trp	Phe	
			275					280					285				
5	Asn	Val	Thr	Phe	Gly	Gly	Gly	Leu	Leu	Cys	Gly	Gly	Ser	Arg	Asn	Pro	
		290					295					300					
	Tyr	Pro	Ala	Ala	Ile	Phe	His	Tyr	Ala	Gly	Ala	Pro	Gly	Gly	Pro	Pro	
	305					310					315					320	
10	Thr	Asp	Glu	Gly	Lys	Ala	Pro	Val	Asp	His	Asn	Cys	Leu	Asp	Leu	Pro	
					325					330					335		
	Asn	Leu	Lys	Pro	Val	Val	Ala	Arg	Asp	Val	Pro	Leu	Ser	Gly	Phe	Ala	
15				340					345					350			
	Lys	Arg	Ala	Asp	Asn	Thr	Leu	Asp	Val	Thr	Leu	Asp	Thr	Thr	Gly	Thr	
			355					360					365				
20	Pro	Leu	Phe	Val	Trp	Lys	Val	Asn	Gly	Ser	Ala	Ile	Asn	Ile	Asp	Trp	
		370					375						380				
	Gly	Arg	Ala	Val	Val	Asp	Tyr	Val	Leu	Thr	Gln	Asn	Thr	Ser	Phe	Pro	
	385					390					395					400	
25	Pro	Gly	Tyr	Asn	Ile	Val	Glu	Val	Asn	Gly	Ala	Asp	Gln	Trp	Ser	Tyr	
					405					410					415		
	Trp	Leu	Ile	Glu	Asn	Asp	Pro	Gly	Ala	Pro	Phe	Thr	Leu	Pro	His	Pro	
30				420					425					430			
	Met	His	Leu	His	Gly	His	Asp	Phe	Tyr	Val	Leu	Gly	Arg	Ser	Pro	Asp	
			435					440					445				
35	Glu	Ser	Pro	Ala	Ser	Asn	Glu	Arg	His	Val	Phe	Asp	Pro	Ala	Arg	Asp	
		450					455					460					
	Ala	Gly	Leu	Leu	Ser	Gly	Ala	Asn	Pro	Val	Arg	Arg	Asp	Val	Ser	Met	
	465					470					475					480	
40	Leu	Pro	Ala	Phe	Gly	Trp	Val	Val	Leu	Ser	Phe	Arg	Ala	Asp	Asn	Pro	
					485					490					495		
	Gly	Ala	Trp	Leu	Phe	His	Cys	His	Ile	Ala	Trp	His	Val	Ser	Gly	Gly	
45				500					505					510			
	Leu	Gly	Val	Val	Tyr	Leu	Glu	Arg	Ala	Asp	Asp	Leu	Arg	Gly	Ala	Val	
			515					520					525				
50	Ser	Asp	Ala	Asp	Ala	Asp	Asp	Leu	Asp	Arg	Leu	Cys	Ala	Asp	Trp	Arg	
		530					535					540					
	Arg	Tyr	Trp	Pro	Thr	Asn	Pro	Tyr	Pro	Lys	Ser	Asp	Ser	Gly	Leu	Lys	
55		545				550					555					560	
	His	Arg	Trp	Val	Glu	Glu	Gly	Glu	Trp	Leu	Val	Lys	Ala				
					565					570							

CLAIMS

1. A method of constructing a variant of a parent *Coprinus* laccase, which variant has laccase activity and improved stability as compared to said parent laccase, which method comprises

i) analysing the structure of the parent *Coprinus* laccase to identify at least one amino acid residue or at least one structural part of the *Coprinus* laccase structure, which amino acid residue or structural part is believed to be of relevance for altering the stability of the parent *Coprinus* laccase (as evaluated on the basis of structural or functional considerations),

15

ii) constructing a *Coprinus* laccase variant, which as compared to the parent *Coprinus* laccase, has been modified in the amino acid residue or structural part identified in i) so as to alter the stability, and, optionally,

20

iii) testing the resulting *Coprinus* laccase variant with respect to stability.

2. The method according to claim 1, wherein the structural part to be modified is at the type I Cu site or at the type III Cu site.

3. A variant of a parent *Coprinus* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 1:

W125,

Y134,

Y126,

Y170,

35 M75, and/or

M477.

4. A method of constructing a variant of a parent *Coprinus*-like

laccase, which variant has laccase activity and improved stability as compared to said parent laccase, which method comprises

- i) comparing the three-dimensional structure of the *Coprinus* laccase with the structure of a *Coprinus*-like laccase,
- ii) identifying a part of the *Coprinus*-like laccase structure which is different from the *Coprinus* laccase structure and which from structural or functional considerations is contemplated to be responsible for differences in the stability of the *Coprinus* and *Coprinus*-like laccase,
- iii) modifying the part of the *Coprinus*-like laccase identified in ii) whereby a *Coprinus*-like laccase variant is obtained, which has an improved stability compared to the parent *Coprinus*-like laccase, and optionally,
- iv) testing the resulting *Coprinus*-like laccase variant with respect to stability.

5. The method according to claim 4, wherein, in step iii), the part of the *Coprinus*-like laccase is modified so as to resemble the corresponding part of the *Coprinus* laccase.

6. The method according to claim 4 or 5, wherein, in step iii), the modification is accomplished by deleting one or more amino acid residues of the part of the *Coprinus*-like laccase to be modified; or the modification is accomplished by replacing one or more amino acid residues of the part of the *Coprinus*-like laccase to be modified with the amino acid residues occupying corresponding positions in the *Coprinus* laccase; or the modification is accomplished by insertion of one or more amino acid residues present in the *Coprinus* laccase into a corresponding position in the *Coprinus*-like laccase.

7. The method according to any of claims 4-6, wherein the *Coprinus*-like laccase is selected from the group consisting of *Polyporus pinsitus* laccase, *Phlebia radiata* laccase, *Rhizoctonia solani* laccase, *Scytalidium thermophilum* laccase

and *Myceliophthora thermophila* laccase.

8. The method according to claim 1 or 4, wherein the parent *Coprinus* laccase is derived from a strain of *Coprinus cinereus*.

5

9. The method according to claim 8, wherein the parent *Coprinus* laccase is derived from *Coprinus cinereus* IFO 8371.

10. A variant of a parent *Polyporus pinsitus* (I) laccase, which
10 comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 2:

W107,

Y116,

Y108,

15 Y152,

M57, and/or

M328.

11. A variant of a parent *Polyporus pinsitus* (II) laccase,
20 which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 3:

W107,

Y116,

Y108,

25 Y152, and/or

M57.

12. A variant of a parent *Phlebia radiata* laccase, which
comprises a mutation in a position corresponding to at least
30 one of the following positions in SEQ ID No. 4:

W128,

Y137,

Y129,

Y137, and/or

35 M78.

13. A variant of a parent *Rhizoctonia solani* (I) laccase, which

comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 5:

W126,
Y135,
5 Y127,
Y171, and/or
M76.

14. A variant of a parent *Rhizoctonia solani* (II) laccase, 10 which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 6:

W439,
W125,
Y134,
15 Y126,
Y170, and/or
M75.

15. A variant of a parent *Rhizoctonia solani* (III) laccase, 20 which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 7:

W411,
W125,
Y134,
25 Y126,
Y170, and/or
M75.

16. A variant of a parent *Rhizoctonia solani* (IV) laccase, 30 which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 8:

W411,
W125,
Y134,
35 Y126,
Y170, and/or
M75.

17. A variant of a parent *Scytalidium thermophilum* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 9:

5 M483,
W422,
W181,
Y190,
M530,
10 Y182,
Y221,
M300, and/or
M313.

15 18. A variant of a parent *Myceliophthora thermophila* laccase, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID No. 10:

W507,
M433,
20 W373,
W136,
Y145,
M480,
Y137,
25 Y176, and/or
M254.

19. A DNA construct comprising a DNA sequence encoding a laccase variant according to claim 3 or claims 10-18.

30

20. A recombinant expression vector which carries a DNA construct according to claim 19.

21. A cell which is transformed with a DNA construct according to claim 19 or a vector according to claim 20.

35

22. A cell according to claim 21, which is a microorganism.

23. A cell according to claim 22, which is a bacterium or a fungus.

5 24. A cell according to claim 23, which is an *Aspergillus niger* or an *Aspergillus oryzae* cell.

25. Use of a laccase variant according to claim 3 or claims 10-18 for oxidizing a substrate.

10

26. Use of a laccase variant according to claim 25 for dye transfer inhibition.

27. Use of a laccase variant according to claim 25 for
15 bleaching textiles, in particular for bleaching denim.

28. A detergent additive comprising a laccase variant according to claim 3 or claims 10-18 in the form of a non-dusting granulate, a stabilised liquid or a protected enzyme.

20

29. A detergent additive according to claim 28, which additionally comprises one or more other enzyme such as a protease, a lipase, an amylase, and/or a cellulase.

25 30. A detergent composition comprising a laccase variant according to claim 3 or claims 10-18 and a surfactant.

31. A detergent composition according to claim 30 which additionally comprises one or more other enzymes such as a
30 protease, a lipase, an amylase and/or a cellulase.

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 97/00571

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C12N 9/02 // (C12N 9/02, C12R 1:645)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 9606930 A1 (NOVO NORDISK A/S), 7 March 1996 (07.03.96)	1-31
X	WO 9600290 A1 (NOVO NORDISK BIOTECH, INC.), 4 January 1996 (04.01.96)	3,10-31
X	WO 9507988 A1 (NOVO NORDISK A/S), 23 March 1995 (23.03.95)	3,10-31
X	WO 9533837 A1 (NOVO NORDISK BIOTECH, INC.), 14 December 1995 (14.12.95)	3,10-31

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents:

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- "E" earlier document but published on or after the international filing date
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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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"&" document member of the same patent family

Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 97/00571

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

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A	WO 9623874 A1 (NOVO NORDISK A/S), 8 August 1996 (08.08.96), see claims and the whole document --	1-2,4-9
A	Biochimica et Biophysica Acta, Volume 1292, 1996, Feng Xu et al, "A study of a series of recombinant fungal laccases and bilirubin oxidase that exhibit significant differences in redox potential, substrate specificity, and stability", page 303 - page 311, page 310 --	1-2,4-9
A	FEMS Microbiology Letters, Volume 132, 1995, Soon-ja Kim et al, "Characteristics of a laccase over-secreting mutant of Coprinus congregatus" page 177 - page 179 -- -----	1-18

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Information on patent family members

02/03/98

International application No.

PCT/DK 97/00571

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